

FILE 'HOME' ENTERED AT 15:42:45 ON 21 JUN 2000

=> fil .bec

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.60	0.60

FILES 'MEDLINE, SCISEARCH, LIFESCI, BIOTECHDS, BIOSIS, EMBASE, HCAPLUS, NTIS,  
ESBIOBASE, BIOTECHNO' ENTERED AT 15:44:57 ON 21 JUN 2000  
ALL COPYRIGHTS AND RESTRICTIONS APPLY. SEE HELP USAGETERMS FOR DETAILS.

## 10 FILES IN THE FILE LIST

=> s carbon (2a) (flux or flow)

```
FILE 'MEDLINE'
      165595 CARBON
      17572 FLUX
      253492 FLOW
L1      511 CARBON(2A) (FLUX OR FLOW)
```

FILE 'SCISEARCH'  
223808 CARBON  
85096 FLUX  
387138 FLOW  
L2 1852 CARBON(2A) (FLUX OR FLOW)

FILE 'LIFESCI'  
34804 CARBON  
8025 FLUX  
35825 FLOW  
L3 735 CARBON(2A) (FLUX OR FLOW)

FILE 'BIOTECHD5'  
8112 CARBON  
1107 FLUX  
9793 FLOW  
14 165 CARBON(2A) (FLUX OR FLOW)

FILE 'BIOSIS'  
199958 CARBON  
35451 FLUX  
272543 FLOW  
L5 2389 CARBON(2A) (FLUX OR FLOW)

FILE 'EMBASE'  
106181 CARBON  
20902 FLUX  
264832 FLOW  
I.6 639 CARBON(2A) (FLUX OR FLOW)

FILE 'HCAPLUS'  
733260 CARBON  
168322 FLUX  
521084 FLOW  
1.7 3658 CARBON(2A) (FLUX OR FLOW)

FILE 'NTIS'  
66895 CARBON  
34694 FLUX  
156247 FLOW  
L8 234 CARBON(2A) (FLUX OR FLOW)

FILE 'ESBIOBASE'  
31445 CARBON  
8657 FLUX  
47993 FLOW  
L9 562 CARBON(2A) (FLUX OR FLOW)

FILE 'BIOTECHNO'  
25115 CARBON  
5096 FLUX  
34964 FLOW  
L10 350 CARBON(2A) (FLUX OR FLOW)

TOTAL FOR ALL FILES  
L11 11095 CARBON(2A) (FLUX OR FLOW)

=> s l11(6a) (modif? or alter? or increas?)

FILE 'MEDLINE'  
247875 MODIF?  
458113 ALTER?  
1365059 INCREAS?  
L12 59 L1 (6A) (MODIF? OR ALTER? OR INCREAS?)

FILE 'SCISEARCH'  
314906 MODIF?  
412512 ALTER?  
1214418 INCREAS?  
L13 116 L2 (6A) (MODIF? OR ALTER? OR INCREAS?)

FILE 'LIFESCI'  
69113 MODIF?  
125281 ALTER?  
359025 INCREAS?  
L14 65 L3 (6A) (MODIF? OR ALTER? OR INCREAS?)

FILE 'BIOTECHDS'  
19630 MODIF?  
14000 ALTER?  
43431 INCREAS?  
L15 30 L4 (6A) (MODIF? OR ALTER? OR INCREAS?)

FILE 'BIOSIS'  
275774 MODIF?  
703175 ALTER?  
1560260 INCREAS?  
L16 141 L5 (6A) (MODIF? OR ALTER? OR INCREAS?)

FILE 'EMBASE'  
239269 MODIF?  
449466 ALTER?  
1353635 INCREAS?  
L17 68 L6 (6A) (MODIF? OR ALTER? OR INCREAS?)

```

FILE 'HCAPLUS'
    588225 MODIF?
    543346 ALTER?
    2542153 INCREAS?
L18      141 L7 (6A) (MODIF? OR ALTER? OR INCREAS?)

FILE 'NTIS'
    91273 MODIF?
    83295 ALTER?
    165754 INCREAS?
L19      9 L8 (6A) (MODIF? OR ALTER? OR INCREAS?)

FILE 'ESBIOBASE'
    70732 MODIF?
    113735 ALTER?
    341323 INCREAS?
L20      52 L9 (6A) (MODIF? OR ALTER? OR INCREAS?)

FILE 'BIOTECHNO'
    60585 MODIF?
    105671 ALTER?
    273906 INCREAS?
L21      38 L10(6A) (MODIF? OR ALTER? OR INCREAS?)

TOTAL FOR ALL FILES
L22      719 L11(6A) (MODIF? OR ALTER? OR INCREAS?)

=> s (phosphoenolpyruvate or (phospho enol or phosphoenol) (w)pyruvate or
     pep) (4a) (suppl#### or availab?)

FILE 'MEDLINE'
    5527 PHOSPHOENOLPYRUVATE
    2515 PHOSPHO
    596 ENOL
    55 PHOSPHO ENOL
        (PHOSPHO(W) ENOL)
    206 PHOSPHOENOL
    20967 PYRUVATE
    2442 PEP
    270502 SUPPL#####
    203666 AVAILAB?
L23      27 (PHOSPHOENOLPYRUVATE OR (PHOSPHO ENOL OR PHOSPHOENOL) (W) PYRUVATE
        OR PEP) (4A) (SUPPL##### OR AVAILAB?)

FILE 'SCISEARCH'
    4795 PHOSPHOENOLPYRUVATE
    1961 PHOSPHO
    5686 ENOL
    58 PHOSPHO ENOL
        (PHOSPHO(W) ENOL)
    187 PHOSPHOENOL
    15215 PYRUVATE
    2080 PEP
    78325 SUPPL#####
    223789 AVAILAB?
L24      35 (PHOSPHOENOLPYRUVATE OR (PHOSPHO ENOL OR PHOSPHOENOL) (W) PYRUVATE
        OR PEP) (4A) (SUPPL##### OR AVAILAB?)

FILE 'LIFESCI'

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1795 PHOSPHOENOLPYRUVATE  
923 "PHOSPHO"  
206 "ENOL"  
17 PHOSPHO ENOL  
("PHOSPHO" (W) "ENOL")  
101 PHOSPHOENOL  
4911 PYRUVATE  
720 PEP  
17032 SUPPL####  
63252 AVAILAB?  
L25 14 (PHOSPHOENOLPYRUVATE OR (PHOSPHO ENOL OR PHOSPHOENOL) (W) PYRUVATE  
OR PEP) (4A) (SUPPL#### OR AVAILAB?)

FILE 'BIOTECHDS'  
304 PHOSPHOENOLPYRUVATE  
142 PHOSPHO  
122 ENOL  
2 PHOSPHO ENOL  
(PHOSPHO (W) ENOL)  
33 PHOSPHOENOL  
1358 PYRUVATE  
141 PEP  
5490 SUPPL####  
5616 AVAILAB?  
L26 6 (PHOSPHOENOLPYRUVATE OR (PHOSPHO ENOL OR PHOSPHOENOL) (W) PYRUVATE  
OR PEP) (4A) (SUPPL#### OR AVAILAB?)

FILE 'BIOSIS'  
6738 PHOSPHOENOLPYRUVATE  
55173 PHOSPHO  
1826 ENOL  
148 PHOSPHO ENOL  
(PHOSPHO (W) ENOL)  
3598 PHOSPHOENOL  
31615 PYRUVATE  
3255 PEP  
82830 SUPPL####  
206349 AVAILAB?  
L27 34 (PHOSPHOENOLPYRUVATE OR (PHOSPHO ENOL OR PHOSPHOENOL) (W) PYRUVATE  
OR PEP) (4A) (SUPPL#### OR AVAILAB?)

FILE 'EMBASE'  
3759 PHOSPHOENOLPYRUVATE  
1882 "PHOSPHO"  
1423 "ENOL"  
38 PHOSPHO ENOL  
("PHOSPHO" (W) "ENOL")  
158 PHOSPHOENOL  
17239 PYRUVATE  
2258 PEP  
62096 SUPPL####  
207328 AVAILAB?  
L28 27 (PHOSPHOENOLPYRUVATE OR (PHOSPHO ENOL OR PHOSPHOENOL) (W) PYRUVATE  
OR PEP) (4A) (SUPPL#### OR AVAILAB?)

FILE 'HCAPLUS'  
9225 PHOSPHOENOLPYRUVATE  
6137 PHOSPHO  
13928 ENOL  
39 PHOSPHO ENOL

(PHOSPHO (W) ENOL)  
493 PHOSPHOENOL  
36233 PYRUVATE  
4793 PEP  
146880 SUPPL####  
269875 AVAILAB?  
L29 55 (PHOSPHOENOLPYRUVATE OR (PHOSPHO ENOL OR PHOSPHOENOL) (W) PYRUVATE  
OR PEP) (4A) (SUPPL#### OR AVAILAB?)

FILE 'NTIS'  
36 PHOSPHOENOLPYRUVATE  
46 PHOSPHO  
74 ENOL  
0 PHOSPHO ENOL  
(PHOSPHO (W) ENOL)  
5 PHOSPHOENOL  
297 PYRUVATE  
1158 PEP  
81632 SUPPL####  
230225 AVAILAB?  
L30 16 (PHOSPHOENOLPYRUVATE OR (PHOSPHO ENOL OR PHOSPHOENOL) (W) PYRUVATE  
OR PEP) (4A) (SUPPL#### OR AVAILAB?)

FILE 'ESBIOBASE'  
1186 PHOSPHOENOLPYRUVATE  
834 PHOSPHO  
263 ENOL  
20 PHOSPHO ENOL  
(PHOSPHO (W) ENOL)  
45 PHOSPHOENOL  
3597 PYRUVATE  
572 PEP  
14145 SUPPL####  
50728 AVAILAB?  
L31 9 (PHOSPHOENOLPYRUVATE OR (PHOSPHO ENOL OR PHOSPHOENOL) (W) PYRUVATE  
OR PEP) (4A) (SUPPL#### OR AVAILAB?)

FILE 'BIOTECHNO'  
1947 PHOSPHOENOLPYRUVATE  
980 PHOSPHO  
149 ENOL  
17 PHOSPHO ENOL  
(PHOSPHO (W) ENOL)  
58 PHOSPHOENOL  
5154 PYRUVATE  
599 PEP  
9608 SUPPL####  
38606 AVAILAB?  
L32 14 (PHOSPHOENOLPYRUVATE OR (PHOSPHO ENOL OR PHOSPHOENOL) (W) PYRUVATE  
OR PEP) (4A) (SUPPL#### OR AVAILAB?)

TOTAL FOR ALL FILES  
L33 237 (PHOSPHOENOLPYRUVATE OR (PHOSPHO ENOL OR PHOSPHOENOL) (W) PYRUVATE  
OR PEP) (4A) (SUPPL#### OR AVAILAB?)

=> s phosphotransferase# or phospho transferase#

FILE 'MEDLINE'  
17143 PHOSPHOTRANSFERASE#  
2515 PHOSPHO

34029 TRANSFERASE#  
14 PHOSPHO TRANSFERASE#  
(PHOSPHO (W) TRANSFERASE#)  
L34 17151 PHOSPHOTRANSFERASE# OR PHOSPHO TRANSFERASE#

FILE 'SCISEARCH'  
3786 PHOSPHOTRANSFERASE#  
1961 PHOSPHO  
27571 TRANSFERASE#  
12 PHOSPHO TRANSFERASE#  
(PHOSPHO (W) TRANSFERASE#)  
L35 3796 PHOSPHOTRANSFERASE# OR PHOSPHO TRANSFERASE#

FILE 'LIFESCI'  
2364 PHOSPHOTRANSFERASE#  
923 "PHOSPHO"  
9714 TRANSFERASE#  
7 PHOSPHO TRANSFERASE#  
("PHOSPHO" (W) TRANSFERASE#)  
L36 2368 PHOSPHOTRANSFERASE# OR PHOSPHO TRANSFERASE#

FILE 'BIOTECHDS'  
1618 PHOSPHOTRANSFERASE#  
142 PHOSPHO  
1549 TRANSFERASE#  
0 PHOSPHO TRANSFERASE#  
(PHOSPHO (W) TRANSFERASE#)  
L37 1618 PHOSPHOTRANSFERASE# OR PHOSPHO TRANSFERASE#

FILE 'BIOSIS'  
5296 PHOSPHOTRANSFERASE#  
55173 PHOSPHO  
58857 TRANSFERASE#  
1749 PHOSPHO TRANSFERASE#  
(PHOSPHO (W) TRANSFERASE#)  
L38 6397 PHOSPHOTRANSFERASE# OR PHOSPHO TRANSFERASE#

FILE 'EMBASE'  
7100 PHOSPHOTRANSFERASE#  
1882 "PHOSPHO"  
25872 TRANSFERASE#  
6 PHOSPHO TRANSFERASE#  
("PHOSPHO" (W) TRANSFERASE#)  
L39 7105 PHOSPHOTRANSFERASE# OR PHOSPHO TRANSFERASE#

FILE 'HCAPLUS'  
6267 PHOSPHOTRANSFERASE#  
6137 PHOSPHO  
33257 TRANSFERASE#  
8 PHOSPHO TRANSFERASE#  
(PHOSPHO (W) TRANSFERASE#)  
L40 6274 PHOSPHOTRANSFERASE# OR PHOSPHO TRANSFERASE#

FILE 'NTIS'  
126 PHOSPHOTRANSFERASE#  
46 PHOSPHO  
713 TRANSFERASE#  
0 PHOSPHO TRANSFERASE#  
(PHOSPHO (W) TRANSFERASE#)  
L41 126 PHOSPHOTRANSFERASE# OR PHOSPHO TRANSFERASE#

FILE 'ESBIOBASE'  
2511 PHOSPHOTRANSFERASE#  
834 PHOSPHO  
19078 TRANSFERASE#  
5 PHOSPHO TRANSFERASE#  
(PHOSPHO (W) TRANSFERASE#)  
L42 2514 PHOSPHOTRANSFERASE# OR PHOSPHO TRANSFERASE#

FILE 'BIOTECHNO'  
4633 PHOSPHOTRANSFERASE#  
980 PHOSPHO  
11638 TRANSFERASE#  
4 PHOSPHO TRANSFERASE#  
(PHOSPHO (W) TRANSFERASE#)  
L43 4635 PHOSPHOTRANSFERASE# OR PHOSPHO TRANSFERASE#

TOTAL FOR ALL FILES  
L44 51984 PHOSPHOTRANSFERASE# OR PHOSPHO TRANSFERASE#

=> s 144 and 111

FILE 'MEDLINE'  
L45 13 L34 AND L1

FILE 'SCISEARCH'  
L46 20 L35 AND L2

FILE 'LIFESCI'  
L47 7 L36 AND L3

FILE 'BIOTECHDS'  
L48 5 L37 AND L4

FILE 'BIOSIS'  
L49 11 L38 AND L5

FILE 'EMBASE'  
L50 8 L39 AND L6

FILE 'HCAPLUS'  
L51 12 L40 AND L7

FILE 'NTIS'  
L52 1 L41 AND L8

FILE 'ESBIOBASE'  
L53 8 L42 AND L9

FILE 'BIOTECHNO'  
L54 8 L43 AND L10

TOTAL FOR ALL FILES  
L55 93 L44 AND L11

=> s 144(8a) (delet? or inactivat?)

FILE 'MEDLINE'  
87427 DELET?  
76530 INACTIVAT?

L56 104 L34(8A) (DELET? OR INACTIVAT?)

FILE 'SCISEARCH'  
71717 DELET?  
58968 INACTIVAT?  
L57 46 L35(8A) (DELET? OR INACTIVAT?)

FILE 'LIFESCI'  
40163 DELET?  
29342 INACTIVAT?  
L58 61 L36(8A) (DELET? OR INACTIVAT?)

FILE 'BIOTECHDS'  
7050 DELET?  
5581 INACTIVAT?  
L59 39 L37(8A) (DELET? OR INACTIVAT?)

FILE 'BIOSIS'  
83620 DELET?  
85386 INACTIVAT?  
L60 109 L38(8A) (DELET? OR INACTIVAT?)

FILE 'EMBASE'  
73850 DELET?  
68050 INACTIVAT?  
L61 73 L39(8A) (DELET? OR INACTIVAT?)

FILE 'HCAPLUS'  
79915 DELET?  
96594 INACTIVAT?  
L62 139 L40(8A) (DELET? OR INACTIVAT?)

FILE 'NTIS'  
4028 DELET?  
1911 INACTIVAT?  
L63 0 L41(8A) (DELET? OR INACTIVAT?)

FILE 'ESBIOBASE'  
32736 DELET?  
21336 INACTIVAT?  
L64 15 L42(8A) (DELET? OR INACTIVAT?)

FILE 'BIOTECHNO'  
52605 DELET?  
29669 INACTIVAT?  
L65 46 L43(8A) (DELET? OR INACTIVAT?)

TOTAL FOR ALL FILES  
L66 632 L44(8A) (DELET? OR INACTIVAT?)

=> s 166 and transport?

FILE 'MEDLINE'  
199769 TRANSPORT?  
L67 9 L56 AND TRANSPORT?

FILE 'SCISEARCH'  
284924 TRANSPORT?  
L68 1 L57 AND TRANSPORT?

FILE 'LIFESCI'  
      54644 TRANSPORT?  
L69      2 L58 AND TRANSPORT?

FILE 'BIOTECHDHS'  
      3396 TRANSPORT?  
L70      1 L59 AND TRANSPORT?

FILE 'BIOSIS'  
      880765 TRANSPORT?  
L71      11 L60 AND TRANSPORT?

FILE 'EMBASE'  
      202138 TRANSPORT?  
L72      9 L61 AND TRANSPORT?

FILE 'HCAPLUS'  
      494433 TRANSPORT?  
L73      16 L62 AND TRANSPORT?

FILE 'NTIS'  
      126980 TRANSPORT?  
L74      0 L63 AND TRANSPORT?

FILE 'ESBIOBASE'  
      110606 TRANSPORT?  
L75      1 L64 AND TRANSPORT?

FILE 'BIOTECHNO'  
      57183 TRANSPORT?  
L76      3 L65 AND TRANSPORT?

TOTAL FOR ALL FILES  
L77      53 L66 AND TRANSPORT?

=> s 144 and glucose

FILE 'MEDLINE'  
      210335 GLUCOSE  
L78      2132 L34 AND GLUCOSE

FILE 'SCISEARCH'  
      131091 GLUCOSE  
L79      676 L35 AND GLUCOSE

FILE 'LIFESCI'  
      33398 GLUCOSE  
L80      418 L36 AND GLUCOSE

FILE 'BIOTECHDHS'  
      24919 GLUCOSE  
L81      81 L37 AND GLUCOSE

FILE 'BIOSIS'  
      217611 GLUCOSE  
L82      1063 L38 AND GLUCOSE

FILE 'EMBASE'  
      169880 GLUCOSE  
L83      851 L39 AND GLUCOSE

FILE 'HCAPLUS'  
L84        245956 GLUCOSE  
              1184 L40 AND GLUCOSE

FILE 'NTIS'  
L85        2781 GLUCOSE  
              9 L41 AND GLUCOSE

FILE 'ESBIOBASE'  
L86        32091 GLUCOSE  
              334 L42 AND GLUCOSE

FILE 'BIOTECHNO'  
L87        32114 GLUCOSE  
              518 L43 AND GLUCOSE

TOTAL FOR ALL FILES  
L88        7266 L44 AND GLUCOSE

=> s 166 and 188

FILE 'MEDLINE'  
L89        15 L56 AND L78

FILE 'SCISEARCH'  
L90        4 L57 AND L79

FILE 'LIFESCI'  
L91        6 L58 AND L80

FILE 'BIOTECHDS'  
L92        4 L59 AND L81

FILE 'BIOSIS'  
L93        16 L60 AND L82

FILE 'EMBASE'  
L94        14 L61 AND L83

FILE 'HCAPLUS'  
L95        19 L62 AND L84

FILE 'NTIS'  
L96        0 L63 AND L85

FILE 'ESBIOBASE'  
L97        3 L64 AND L86

FILE 'BIOTECHNO'  
L98        7 L65 AND L87

TOTAL FOR ALL FILES  
L99        88 L66 AND L88

=> s 188 and transport

FILE 'MEDLINE'  
L100      169094 TRANSPORT  
              590 L78 AND TRANSPORT

FILE 'SCISEARCH'  
    252462 TRANSPORT  
L101       303 L79 AND TRANSPORT

FILE 'LIFESCI'  
    44285 TRANSPORT  
L102       165 L80 AND TRANSPORT

FILE 'BIOTECHDS'  
    2625 TRANSPORT  
L103       16 L81 AND TRANSPORT

FILE 'BIOSIS'  
    853558 TRANSPORT  
L104       356 L82 AND TRANSPORT

FILE 'EMBASE'  
    183212 TRANSPORT  
L105       373 L83 AND TRANSPORT

FILE 'HCAPLUS'  
    445874 TRANSPORT  
L106       486 L84 AND TRANSPORT

FILE 'NTIS'  
    73937 TRANSPORT  
L107       3 L85 AND TRANSPORT

FILE 'ESBIOBASE'  
    103397 TRANSPORT  
L108       162 L86 AND TRANSPORT

FILE 'BIOTECHNO'  
    50543 TRANSPORT  
L109       248 L87 AND TRANSPORT

TOTAL FOR ALL FILES  
L110       2702 L88 AND TRANSPORT

=> s l110 and (phosphoenolpyruvate or (phospho enol or phosphoenol) (w)pyruvate or pep)

FILE 'MEDLINE'  
    5527 PHOSPHOENOLPYRUVATE  
    2515 PHOSPHO  
    596 ENOL  
    55 PHOSPHO ENOL  
        (PHOSPHO(W) ENOL)  
    206 PHOSPHOENOL  
    20967 PYRUVATE  
        230 (PHOSPHO ENOL OR PHOSPHOENOL) (W) PYRUVATE  
    2442 PEP  
L111       310 L100 AND (PHOSPHOENOLPYRUVATE OR (PHOSPHO ENOL OR PHOSPHOENOL) (W  
            ) PYRUVATE OR PEP)

FILE 'SCISEARCH'  
    4795 PHOSPHOENOLPYRUVATE  
    1961 PHOSPHO  
    5686 ENOL

58 PHOSPHO ENOL  
(PHOSPHO(W) ENOL)  
187 PHOSPHOENOL  
15215 PYRUVATE  
228 (PHOSPHO ENOL OR PHOSPHOENOL) (W) PYRUVATE  
2080 PEP  
L112 206 L101 AND (PHOSPHOENOLPYRUVATE OR (PHOSPHO ENOL OR PHOSPHOENOL) (W  
) PYRUVATE OR PEP)

FILE 'LIFESCI'  
1795 PHOSPHOENOLPYRUVATE  
923 "PHOSPHO"  
206 "ENOL"  
17 PHOSPHO ENOL  
("PHOSPHO" (W) "ENOL")  
101 PHOSPHOENOL  
4911 PYRUVATE  
108 (PHOSPHO ENOL OR PHOSPHOENOL) (W) PYRUVATE  
720 PEP  
L113 120 L102 AND (PHOSPHOENOLPYRUVATE OR (PHOSPHO ENOL OR PHOSPHOENOL) (W  
) PYRUVATE OR PEP)

FILE 'BIOTECHDS'  
304 PHOSPHOENOLPYRUVATE  
142 PHOSPHO  
122 ENOL  
2 PHOSPHO ENOL  
(PHOSPHO(W) ENOL)  
33 PHOSPHOENOL  
1358 PYRUVATE  
32 (PHOSPHO ENOL OR PHOSPHOENOL) (W) PYRUVATE  
141 PEP  
L114 10 L103 AND (PHOSPHOENOLPYRUVATE OR (PHOSPHO ENOL OR PHOSPHOENOL) (W  
) PYRUVATE OR PEP)

FILE 'BIOSIS'  
6738 PHOSPHOENOLPYRUVATE  
55173 PHOSPHO  
1826 ENOL  
148 PHOSPHO ENOL  
(PHOSPHO(W) ENOL)  
3598 PHOSPHOENOL  
31615 PYRUVATE  
3685 (PHOSPHO ENOL OR PHOSPHOENOL) (W) PYRUVATE  
3255 PEP  
L115 241 L104 AND (PHOSPHOENOLPYRUVATE OR (PHOSPHO ENOL OR PHOSPHOENOL) (W  
) PYRUVATE OR PEP)

FILE 'EMBASE'  
3759 PHOSPHOENOLPYRUVATE  
1882 "PHOSPHO"  
1423 "ENOL"  
38 PHOSPHO ENOL  
("PHOSPHO" (W) "ENOL")  
158 PHOSPHOENOL  
17239 PYRUVATE  
179 (PHOSPHO ENOL OR PHOSPHOENOL) (W) PYRUVATE  
2258 PEP  
L116 234 L105 AND (PHOSPHOENOLPYRUVATE OR (PHOSPHO ENOL OR PHOSPHOENOL) (W  
) PYRUVATE OR PEP)

FILE 'HCAPLUS'  
9225 PHOSPHOENOLPYRUVATE  
6137 PHOSPHO  
13928 ENOL  
39 PHOSPHO ENOL  
(PHOSPHO (W) ENOL)  
493 PHOSPHOENOL  
36233 PYRUVATE  
466 (PHOSPHO ENOL OR PHOSPHOENOL) (W) PYRUVATE  
4793 PEP  
L117 362 L106 AND (PHOSPHOENOLPYRUVATE OR (PHOSPHO ENOL OR PHOSPHOENOL) (W)  
) PYRUVATE OR PEP)

FILE 'NTIS'  
36 PHOSPHOENOLPYRUVATE  
46 PHOSPHO  
74 ENOL  
0 PHOSPHO ENOL  
(PHOSPHO (W) ENOL)  
5 PHOSPHOENOL  
297 PYRUVATE  
3 (PHOSPHO ENOL OR PHOSPHOENOL) (W) PYRUVATE  
1158 PEP  
L118 3 L107 AND (PHOSPHOENOLPYRUVATE OR (PHOSPHO ENOL OR PHOSPHOENOL) (W)  
) PYRUVATE OR PEP)

FILE 'ESBIOBASE'  
1186 PHOSPHOENOLPYRUVATE  
834 PHOSPHO  
263 ENOL  
20 PHOSPHO ENOL  
(PHOSPHO (W) ENOL)  
45 PHOSPHOENOL  
3597 PYRUVATE  
63 (PHOSPHO ENOL OR PHOSPHOENOL) (W) PYRUVATE  
572 PEP  
L119 84 L108 AND (PHOSPHOENOLPYRUVATE OR (PHOSPHO ENOL OR PHOSPHOENOL) (W)  
) PYRUVATE OR PEP)

FILE 'BIOTECHNO'  
1947 PHOSPHOENOLPYRUVATE  
980 PHOSPHO  
149 ENOL  
17 PHOSPHO ENOL  
(PHOSPHO (W) ENOL)  
58 PHOSPHOENOL  
5154 PYRUVATE  
69 (PHOSPHO ENOL OR PHOSPHOENOL) (W) PYRUVATE  
599 PEP  
L120 157 L109 AND (PHOSPHOENOLPYRUVATE OR (PHOSPHO ENOL OR PHOSPHOENOL) (W)  
) PYRUVATE OR PEP)

TOTAL FOR ALL FILES  
L121 1727 L110 AND (PHOSPHOENOLPYRUVATE OR (PHOSPHO ENOL OR PHOSPHOENOL) (W)  
) PYRUVATE OR PEP)

=> s 1121 and mut/q

FILE 'MEDLINE'

L122 194 L111 AND MUT/Q

FILE 'SCISEARCH'  
L123 122 L112 AND MUT/Q

FILE 'LIFESCI'  
L124 61 L113 AND MUT/Q

FILE 'BIOTECHDS'  
L125 8 L114 AND MUT/Q

FILE 'BIOSIS'  
L126 134 L115 AND MUT/Q

FILE 'EMBASE'  
L127 131 L116 AND MUT/Q

FILE 'HCAPLUS'  
L128 187 L117 AND MUT/Q

FILE 'NTIS'  
L129 2 L118 AND MUT/Q

FILE 'ESBIOBASE'  
L130 53 L119 AND MUT/Q

FILE 'BIOTECHNO'  
L131 95 L120 AND MUT/Q

TOTAL FOR ALL FILES  
L132 987 L121 AND MUT/Q

=> s l132 and (aromatic or shikimate)

FILE 'MEDLINE'  
20282 AROMATIC  
282 SHIKIMATE  
L133 2 L122 AND (AROMATIC OR SHIKIMATE)

FILE 'SCISEARCH'  
67941 AROMATIC  
640 SHIKIMATE  
L134 3 L123 AND (AROMATIC OR SHIKIMATE)

FILE 'LIFESCI'  
10616 AROMATIC  
228 SHIKIMATE  
L135 2 L124 AND (AROMATIC OR SHIKIMATE)

FILE 'BIOTECHDS'  
4057 AROMATIC  
86 SHIKIMATE  
L136 1 L125 AND (AROMATIC OR SHIKIMATE)

FILE 'BIOSIS'  
37167 AROMATIC  
957 SHIKIMATE  
L137 2 L126 AND (AROMATIC OR SHIKIMATE)

FILE 'EMBASE'

32677 AROMATIC  
239 SHIKIMATE  
L138 2 L127 AND (AROMATIC OR SHIKIMATE)

FILE 'HCAPLUS'  
127299 AROMATIC  
222721 AROM  
272472 AROMATIC  
(AROMATIC OR AROM)  
1406 SHIKIMATE  
L139 4 L128 AND (AROMATIC OR SHIKIMATE)

FILE 'NTIS'  
10987 AROMATIC  
8 SHIKIMATE  
L140 0 L129 AND (AROMATIC OR SHIKIMATE)

FILE 'ESBIOBASE'  
8986 AROMATIC  
168 SHIKIMATE  
L141 1 L130 AND (AROMATIC OR SHIKIMATE)

FILE 'BIOTECHNO'  
9121 AROMATIC  
158 SHIKIMATE  
L142 2 L131 AND (AROMATIC OR SHIKIMATE)

TOTAL FOR ALL FILES  
L143 19 L132 AND (AROMATIC OR SHIKIMATE)

=> s 122 and (phosphoenolpyruvate or (phospho enol or phosphoenol) (w)pyruvate or pep)

FILE 'MEDLINE'  
5527 PHOSPHOENOLPYRUVATE  
2515 PHOSPHO  
596 ENOL  
55 PHOSPHO ENOL  
(PHOSPHO (W) ENOL)  
206 PHOSPHOENOL  
20967 PYRUVATE  
230 (PHOSPHO ENOL OR PHOSPHOENOL) (W) PYRUVATE  
2442 PEP  
L144 6 L12 AND (PHOSPHOENOLPYRUVATE OR (PHOSPHO ENOL OR PHOSPHOENOL) (W)  
PYRUVATE OR PEP)

FILE 'SCISEARCH'  
4795 PHOSPHOENOLPYRUVATE  
1961 PHOSPHO  
5686 ENOL  
58 PHOSPHO ENOL  
(PHOSPHO (W) ENOL)  
187 PHOSPHOENOL  
15215 PYRUVATE  
228 (PHOSPHO ENOL OR PHOSPHOENOL) (W) PYRUVATE  
2080 PEP  
L145 9 L13 AND (PHOSPHOENOLPYRUVATE OR (PHOSPHO ENOL OR PHOSPHOENOL) (W)  
PYRUVATE OR PEP)

FILE 'LIFESCI'

1795 PHOSPHOENOLPYRUVATE  
923 "PHOSPHO"  
206 "ENOL"  
17 PHOSPHO ENOL  
("PHOSPHO" (W) "ENOL")  
101 PHOSPHOENOL  
4911 PYRUVATE  
108 (PHOSPHO ENOL OR PHOSPHOENOL) (W) PYRUVATE  
720 PEP  
L146 8 L14 AND (PHOSPHOENOLPYRUVATE OR (PHOSPHO ENOL OR PHOSPHOENOL) (W)  
PYRUVATE OR PEP)

FILE 'BIOTECHDS'  
304 PHOSPHOENOLPYRUVATE  
142 PHOSPHO  
122 ENOL  
2 PHOSPHO ENOL  
(PHOSPHO (W) ENOL)  
33 PHOSPHOENOL  
1358 PYRUVATE  
32 (PHOSPHO ENOL OR PHOSPHOENOL) (W) PYRUVATE  
141 PEP  
L147 5 L15 AND (PHOSPHOENOLPYRUVATE OR (PHOSPHO ENOL OR PHOSPHOENOL) (W)  
PYRUVATE OR PEP)

FILE 'BIOSIS'  
6738 PHOSPHOENOLPYRUVATE  
55173 PHOSPHO  
1826 ENOL  
148 PHOSPHO ENOL  
(PHOSPHO (W) ENOL)  
3598 PHOSPHOENOL  
31615 PYRUVATE  
3685 (PHOSPHO ENOL OR PHOSPHOENOL) (W) PYRUVATE  
3255 PEP  
L148 14 L16 AND (PHOSPHOENOLPYRUVATE OR (PHOSPHO ENOL OR PHOSPHOENOL) (W)  
PYRUVATE OR PEP)

FILE 'EMBASE'  
3759 PHOSPHOENOLPYRUVATE  
1882 "PHOSPHO"  
1423 "ENOL"  
38 PHOSPHO ENOL  
("PHOSPHO" (W) "ENOL")  
158 PHOSPHOENOL  
17239 PYRUVATE  
179 (PHOSPHO ENOL OR PHOSPHOENOL) (W) PYRUVATE  
2258 PEP  
L149 6 L17 AND (PHOSPHOENOLPYRUVATE OR (PHOSPHO ENOL OR PHOSPHOENOL) (W)  
PYRUVATE OR PEP)

FILE 'HCAPLUS'  
9225 PHOSPHOENOLPYRUVATE  
6137 PHOSPHO  
13928 ENOL  
39 PHOSPHO ENOL  
(PHOSPHO (W) ENOL)  
493 PHOSPHOENOL  
36233 PYRUVATE  
466 (PHOSPHO ENOL OR PHOSPHOENOL) (W) PYRUVATE

4793 PEP  
L150 16 L18 AND (PHOSPHOENOLPYRUVATE OR (PHOSPHO ENOL OR PHOSPHOENOL) (W)  
PYRUVATE OR PEP)

FILE 'NTIS'  
36 PHOSPHOENOLPYRUVATE  
46 PHOSPHO  
74 ENOL  
0 PHOSPHO ENOL  
(PHOSPHO(W) ENOL)  
5 PHOSPHOENOL  
297 PYRUVATE  
3 (PHOSPHO ENOL OR PHOSPHOENOL) (W) PYRUVATE  
1158 PEP  
L151 0 L19 AND (PHOSPHOENOLPYRUVATE OR (PHOSPHO ENOL OR PHOSPHOENOL) (W)  
PYRUVATE OR PEP)

FILE 'ESBIOBASE'  
1186 PHOSPHOENOLPYRUVATE  
834 PHOSPHO  
263 ENOL  
20 PHOSPHO ENOL  
(PHOSPHO(W) ENOL)  
45 PHOSPHOENOL  
3597 PYRUVATE  
63 (PHOSPHO ENOL OR PHOSPHOENOL) (W) PYRUVATE  
572 PEP  
L152 6 L20 AND (PHOSPHOENOLPYRUVATE OR (PHOSPHO ENOL OR PHOSPHOENOL) (W)  
PYRUVATE OR PEP)

FILE 'BIOTECHNO'  
1947 PHOSPHOENOLPYRUVATE  
980 PHOSPHO  
149 ENOL  
17 PHOSPHO ENOL  
(PHOSPHO(W) ENOL)  
58 PHOSPHOENOL  
5154 PYRUVATE  
69 (PHOSPHO ENOL OR PHOSPHOENOL) (W) PYRUVATE  
599 PEP  
L153 6 L21 AND (PHOSPHOENOLPYRUVATE OR (PHOSPHO ENOL OR PHOSPHOENOL) (W)  
PYRUVATE OR PEP)

TOTAL FOR ALL FILES  
L154 76 L22 AND (PHOSPHOENOLPYRUVATE OR (PHOSPHO ENOL OR PHOSPHOENOL) (W)  
PYRUVATE OR PEP)

=> s 122 and glucose

FILE 'MEDLINE'  
210335 GLUCOSE  
L155 22 L12 AND GLUCOSE

FILE 'SCISEARCH'  
131091 GLUCOSE  
L156 23 L13 AND GLUCOSE

FILE 'LIFESCI'  
33398 GLUCOSE  
L157 13 L14 AND GLUCOSE

FILE 'BIOTECHDS'  
24919 GLUCOSE  
L158 13 L15 AND GLUCOSE

FILE 'BIOSIS'  
217611 GLUCOSE  
L159 31 L16 AND GLUCOSE

FILE 'EMBASE'  
169880 GLUCOSE  
L160 28 L17 AND GLUCOSE

FILE 'HCAPLUS'  
245956 GLUCOSE  
L161 28 L18 AND GLUCOSE

FILE 'NTIS'  
2781 GLUCOSE  
L162 0 L19 AND GLUCOSE

FILE 'ESBIOBASE'  
32091 GLUCOSE  
L163 14 L20 AND GLUCOSE

FILE 'BIOTECHNO'  
32114 GLUCOSE  
L164 18 L21 AND GLUCOSE

TOTAL FOR ALL FILES  
L165 190 L22 AND GLUCOSE

=> s (133 or 155 or 177 or 199 or 1132 or 1143 or 1154 or 1165) and py=<1995  
range=1998,

FILE 'MEDLINE'  
7783 PY=<1995  
L166 0 (L23 OR L45 OR L67 OR L89 OR L122 OR L133 OR L144 OR L155) AND  
PY=<1995

FILE 'SCISEARCH'  
76 PY=<1995  
L167 0 (L24 OR L46 OR L68 OR L90 OR L123 OR L134 OR L145 OR L156) AND  
PY=<1995

FILE 'LIFESCI'  
2457 PY=<1995  
L168 0 (L25 OR L47 OR L69 OR L91 OR L124 OR L135 OR L146 OR L157) AND  
PY=<1995

FILE 'BIOTECHDS'  
25 PY=<1995  
(PY=<1995)  
L169 0 (L26 OR L48 OR L70 OR L92 OR L125 OR L136 OR L147 OR L158) AND  
PY=<1995

FILE 'BIOSIS'  
1354 PY=<1995  
L170 0 (L27 OR L49 OR L71 OR L93 OR L126 OR L137 OR L148 OR L159) AND  
PY=<1995

FILE 'EMBASE'  
L171 81 PY=<1995  
0 (L28 OR L50 OR L72 OR L94 OR L127 OR L138 OR L149 OR L160) AND  
PY=<1995

FILE 'HCAPLUS'  
L172 6507 PY=<1995  
0 (L29 OR L51 OR L73 OR L95 OR L128 OR L139 OR L150 OR L161) AND  
PY=<1995

FILE 'NTIS'  
L173 47041 PY=<1995  
0 (L30 OR L52 OR L74 OR L96 OR L129 OR L140 OR L151 OR L162) AND  
PY=<1995

FILE 'ESBIOBASE'  
L174 0 PY=<1995  
0 (L31 OR L53 OR L75 OR L97 OR L130 OR L141 OR L152 OR L163) AND  
PY=<1995

FILE 'BIOTECHNO'  
L175 845083 PY=<1995  
75 (L32 OR L54 OR L76 OR L98 OR L131 OR L142 OR L153 OR L164) AND  
PY=<1995

TOTAL FOR ALL FILES  
L176 75 (L33 OR L55 OR L77 OR L99 OR L132 OR L143 OR L154 OR L165) AND  
PY=<1995

=> dup rem 1176

PROCESSING COMPLETED FOR L176  
L177 75 DUP REM L176 (0 DUPLICATES REMOVED)

=> d tot

L177 ANSWER 1 OF 75 BIOTECHNO COPYRIGHT 2000 Elsevier Science B.V.  
TI Glucose kinase-dependent catabolite repression in  
Staphylococcus xylosus  
SO Journal of Bacteriology, (1995), 177/21 (6144-6152)  
CODEN: JOBAAY ISSN: 0021-9193  
AU Wagner E.; Marcandier S.; Egster O.; Deutscher J.; Gotz F.; Bruckner R.  
AN 1995:25326230 BIOTECHNO

L177 ANSWER 2 OF 75 BIOTECHNO COPYRIGHT 2000 Elsevier Science B.V.  
TI Regulation of sugar **transport** via the multiple sugar metabolism  
operon of Streptococcus **mutans** by the  
**phosphoenolpyruvate phosphotransferase** system  
SO Journal of Bacteriology, (1995), 177/19 (5704-5706)  
CODEN: JOBAAY ISSN: 0021-9193  
AU Cvitkovitch D.G.; Boyd D.A.; Hamilton I.R.  
AN 1995:26028884 BIOTECHNO

L177 ANSWER 3 OF 75 BIOTECHNO COPYRIGHT 2000 Elsevier Science B.V.  
TI Use of feedback-resistant threonine dehydratases of *Corynebacterium*  
glutamicum to **increase carbon flux** towards  
L-isoleucine  
SO Applied and Environmental Microbiology, (1995), 61/12

(4315-4320)  
CODEN: AEMIDF ISSN: 0099-2240  
AU Morbach S.; Sahm H.; Eggeling L.  
AN 1995:25361670 BIOTECHNO

L177 ANSWER 4 OF 75 BIOTECHNO COPYRIGHT 2000 Elsevier Science B.V.  
TI Regulation of ATP-dependent P-(Ser)-HPr formation in *Streptococcus mutans* and *Streptococcus salivarius*  
SO *Journal of Bacteriology*, (1995), 177/10 (2751-2759)  
CODEN: JOBAAY ISSN: 0021-9193  
AU Thevenot T.; Brochu D.; Vadeboncoeur C.; Hamilton I.R.  
AN 1995:25148797 BIOTECHNO

L177 ANSWER 5 OF 75 BIOTECHNO COPYRIGHT 2000 Elsevier Science B.V.  
TI Sequence, expression, and function of the gene for the nonphosphorylating, NADP-dependent glyceraldehyde-3-phosphate dehydrogenase of *Streptococcus mutans*  
SO *Journal of Bacteriology*, (1995), 177/10 (2622-2627)  
CODEN: JOBAAY ISSN: 0021-9193  
AU Boyd D.A.; Cvitkovitch D.G.; Hamilton I.R.  
AN 1995:25148781 BIOTECHNO

L177 ANSWER 6 OF 75 BIOTECHNO COPYRIGHT 2000 Elsevier Science B.V.  
TI Regulation of the lactose **phosphotransferase** system of *Streptococcus bovis* by **glucose**: Independence of inducer exclusion and expulsion mechanisms  
SO *Microbiology*, (1995), 141/9 (2261-2269)  
CODEN: MROBEO ISSN: 1350-0872  
AU Cook G.M.; Kearns D.B.; Russell J.B.; Reizer J.; Saier Jr. M.H.  
AN 1995:25303431 BIOTECHNO

L177 ANSWER 7 OF 75 BIOTECHNO COPYRIGHT 2000 Elsevier Science B.V.  
TI **Glucose transport** by a **mutant** of *Streptococcus mutans* unable to accumulate sugars via the **phosphoenolpyruvate phosphotransferase** system  
SO *Journal of Bacteriology*, (1995), 177/9 (2251-2258)  
CODEN: JOBAAY ISSN: 0021-9193  
AU Cvitkovitch D.G.; Boyd D.A.; Thevenot T.; Hamilton I.R.  
AN 1995:25144127 BIOTECHNO

L177 ANSWER 8 OF 75 BIOTECHNO COPYRIGHT 2000 Elsevier Science B.V.  
TI Regulation of bacterial sugar-H.<sup>sup.+</sup> symport by **phosphoenolpyruvate**-dependent enzyme I/HPr-mediated phosphorylation  
SO *Proceedings of the National Academy of Sciences of the United States of America*, (1995), 92/3 (778-782)  
CODEN: PNASA6 ISSN: 0027-8424  
AU Poolman B.; Knol J.; Mollet B.; Nieuwenhuis B.; Sulter G.  
AN 1995:25048792 BIOTECHNO

L177 ANSWER 9 OF 75 BIOTECHNO COPYRIGHT 2000 Elsevier Science B.V.  
TI In *Saccharomyces cerevisiae* deletion of phosphoglucose isomerase can be suppressed by increased activities of enzymes of the hexose monophosphate pathway  
SO *Microbiology*, (1995), 141/2 (385-391)  
CODEN: MROBEO ISSN: 1350-0872  
AU Dickinson J.R.; Sobanski M.A.; Hewlins M.J.E.  
AN 1995:25070660 BIOTECHNO

L177 ANSWER 10 OF 75 BIOTECHNO COPYRIGHT 2000 Elsevier Science B.V.

TI How neutral red **modified carbon** and electron  
flow in *Clostridium acetobutylicum* grown in chemostat culture at  
neutral pH

SO FEMS Microbiology Reviews, (1995), 16/2-3 (151-162)  
CODEN: FMREE4 ISSN: 0168-6445

AU Girbal L.; Vasconcelos I.; Saint-Amans S.; Soucaille P.

AN 1995:25068038 BIOTECHNO

L177 ANSWER 11 OF 75 BIOTECHNO COPYRIGHT 2000 Elsevier Science B.V.

TI Improved strains of recombinant *Escherichia coli* for ethanol production  
from sugar mixtures

SO Applied Microbiology and Biotechnology, (1995), 43/1 (70-75)  
CODEN: AMBIDG ISSN: 0175-7598

AU Lindsay S.E.; Bothast R.J.; Ingram L.O.

AN 1995:25138872 BIOTECHNO

L177 ANSWER 12 OF 75 BIOTECHNO COPYRIGHT 2000 Elsevier Science B.V.

TI Inhibition of the **phosphoenolpyruvate:lactose**  
**phosphotransferase** system and activation of a cytoplasmic  
sugar-phosphate phosphatase in *Lactococcus lactis* by ATP-dependent  
metabolite-activated phosphorylation of serine 46 in the phosphocarrier  
protein HPr

SO Journal of Biological Chemistry, (1994), 269/16 (11837-11844)  
CODEN: JBCHA3 ISSN: 0021-9258

AU Jing Jing Ye; Reizer J.; Cui X.; Saier Jr. M.H.

AN 1994:24196670 BIOTECHNO

L177 ANSWER 13 OF 75 BIOTECHNO COPYRIGHT 2000 Elsevier Science B.V.

TI The role of phosphoenolpyruvate in the simultaneous uptake of fructose  
and 2-deoxyglucose by *Escherichia coli*

SO Proceedings of the National Academy of Sciences of the United States of  
America, (1994), 91/23 (11080-11083)  
CODEN: PNASA6 ISSN: 0027-8424

AU Kornberg H.; Lambourne L.T.M.

AN 1994:24349629 BIOTECHNO

L177 ANSWER 14 OF 75 BIOTECHNO COPYRIGHT 2000 Elsevier Science B.V.

TI Characterization of a **glucose transport** system in  
*Vibrio parahaemolyticus*

SO Journal of Bacteriology, (1994), 176/23 (7378-7382)  
CODEN: JOBAAY ISSN: 0021-9193

AU Sarker R.I.; Ogawa W.; Tsuda M.; Tanaka S.; Tsuchiya T.

AN 1994:24364067 BIOTECHNO

L177 ANSWER 15 OF 75 BIOTECHNO COPYRIGHT 2000 Elsevier Science B.V.

TI Engineering of *Escherichia coli* central metabolism for **aromatic**  
metabolite production with near theoretical yield

SO Applied and Environmental Microbiology, (1994), 60/11  
(3903-3908)  
CODEN: AEMIDF ISSN: 0099-2240

AU Patnaik R.; Liao J.C.

AN 1994:24335837 BIOTECHNO

L177 ANSWER 16 OF 75 BIOTECHNO COPYRIGHT 2000 Elsevier Science B.V.

TI Regulation of 2-deoxyglucose phosphate accumulation in *Lactococcus lactis*  
vesicles by metabolite-activated, ATP-dependent phosphorylation of  
serine-46 in HPr of the **phosphotransferase** system

SO Microbiology, (1994), 140/12 (3421-3429)  
CODEN: MROBEO ISSN: 1350-0872

AU Ye J.J.; Reizer J.; Saier Jr. M.H.

AN 1994:25020629 BIOTECHNO

L177 ANSWER 17 OF 75 BIOTECHNO COPYRIGHT 2000 Elsevier Science B.V.  
TI Loss of protein kinase-catalyzed phosphorylation of HPr, a phosphocarrier protein of the **phosphotransferase** system, by **mutation**  
of the ptsH gene confers catabolite repression resistance to several catabolic genes of *Bacillus subtilis*  
SO *Journal of Bacteriology*, (1994), 176/11 (3336-3344)  
CODEN: JOBAAY ISSN: 0021-9193  
AU Deutscher J.; Reizer J.; Fischer C.; Galinier A.; Saier Jr. M.H.; Steinmetz M.  
AN 1994:24166726 BIOTECHNO

L177 ANSWER 18 OF 75 BIOTECHNO COPYRIGHT 2000 Elsevier Science B.V.  
TI Vesicles prepared from *Streptococcus mutans* demonstrate the presence of a second **glucose transport** system  
SO *Microbiology*, (1994), 140/10 (2639-2648)  
CODEN: MROBEO ISSN: 1350-0872  
AU Buckley N.D.; Hamilton I.R.  
AN 1994:24326662 BIOTECHNO

L177 ANSWER 19 OF 75 BIOTECHNO COPYRIGHT 2000 Elsevier Science B.V.  
TI Mechanism of catabolite repression of tryptophanase synthesis in *Escherichia coli*  
SO *Microbiology*, (1994), 140/8 (2125-2134)  
CODEN: MROBEO ISSN: 1350-0872  
AU Isaacs Jr H.; Chao D.; Yanofsky C.; Saier Jr M.H.  
AN 1994:24259050 BIOTECHNO

L177 ANSWER 20 OF 75 BIOTECHNO COPYRIGHT 2000 Elsevier Science B.V.  
TI Genetic regulation of fructosyltransferase in *Streptococcus mutans*  
SO *Infection and Immunity*, (1994), 62/4 (1241-1251)  
CODEN: INFIBR ISSN: 0019-9567  
AU Kiska D.L.; Macrina F.L.  
AN 1994:24110816 BIOTECHNO

L177 ANSWER 21 OF 75 BIOTECHNO COPYRIGHT 2000 Elsevier Science B.V.  
TI Sequence and expression of the genes for HPr (ptsH) and enzyme I (ptsI) of the **phosphoenolpyruvate-dependent phosphotransferase transport** system from *Streptococcus mutans*  
SO *Infection and Immunity*, (1994), 62/4 (1156-1165)  
CODEN: INFIBR ISSN: 0019-9567  
AU Boyd D.A.; Cvitkovitch D.G.; Hamilton I.R.  
AN 1994:24110804 BIOTECHNO

L177 ANSWER 22 OF 75 BIOTECHNO COPYRIGHT 2000 Elsevier Science B.V.  
TI **Glucose transport** by the **phosphoenolpyruvate** : Mannose **phosphotransferase** system in *Lactobacillus casei* ATCC 393 and its role in carbon catabolite repression  
SO *Microbiology*, (1994), 140/5 (1141-1149)  
CODEN: MROBEO ISSN: 1350-0872  
AU Veyrat A.; Monedero V.; Perez-Martinez G.  
AN 1994:24157864 BIOTECHNO

L177 ANSWER 23 OF 75 BIOTECHNO COPYRIGHT 2000 Elsevier Science B.V.  
TI The **glucose**-starvation stimulon of *Escherichia coli*: Induced and repressed synthesis of enzymes of central metabolic pathways and role of acetyl phosphate in gene expression and starvation survival  
SO *Molecular Microbiology*, (1994), 12/5 (833-843)  
CODEN: MOMIEE ISSN: 0950-382X

AU Nystrom T.  
AN 1994:24214476 BIOTECHNO

L177 ANSWER 24 OF 75 BIOTECHNO COPYRIGHT 2000 Elsevier Science B.V.  
TI Alteration of the biochemical valves in the central metabolism of  
escherichia coli  
SO Annals of the New York Academy of Sciences, (1994), 745/-  
(21-34)  
CODEN: ANYAA0 ISSN: 0077-8923

AU Liao J.C.; Chao Y.-P.; Patnaik R.  
AN 1994:26005842 BIOTECHNO

L177 ANSWER 25 OF 75 BIOTECHNO COPYRIGHT 2000 Elsevier Science B.V.  
TI Alteration of growth yield by overexpression of  
**phosphoenolpyruvate** carboxylase and **phosphoenolpyruvate**  
carboxykinase in Escherichia coli  
SO Applied and Environmental Microbiology, (1993), 59/12  
(4261-4265)  
CODEN: AEMIDF ISSN: 0099-2240

AU Chao Y.-P.; Liao J.C.  
AN 1993:23361415 BIOTECHNO

L177 ANSWER 26 OF 75 BIOTECHNO COPYRIGHT 2000 Elsevier Science B.V.  
TI Effects of N-acetylglucosamine on carbohydrate fermentation by  
Streptococcus **mutans** NCTC 10449 and Streptococcus sobrinus SL-1  
SO Infection and Immunity, (1993), 61/1 (295-302)  
CODEN: INFIBR ISSN: 0019-9567

AU Homer K.A.; Patel R.; Beighton D.  
AN 1993:23015430 BIOTECHNO

L177 ANSWER 27 OF 75 BIOTECHNO COPYRIGHT 2000 Elsevier Science B.V.  
TI Functional interactions between proteins of the  
**phosphoenolpyruvate**:sugar **phosphotransferase** systems of  
Bacillus subtilis and Escherichia coli  
SO Journal of Biological Chemistry, (1992), 267/13 (9158-9169)  
CODEN: JBCHA3 ISSN: 0021-9258

AU Reizer J.; Sutrina S.L.; Wu L.-F.; Deutscher J.; Reddy P.; Saier Jr. M.H.  
AN 1992:22282071 BIOTECHNO

L177 ANSWER 28 OF 75 BIOTECHNO COPYRIGHT 2000 Elsevier Science B.V.  
TI Lithium inhibits hepatic gluconeogenesis and **phosphoenolpyruvate**  
carboxykinase gene expression  
SO Journal of Biological Chemistry, (1992), 267/5 (2888-2893)  
CODEN: JBCHA3 ISSN: 0021-9258

AU Bosch F.; Rodriguez-Gil J.E.; Hatzoglou M.; Gomez-Foix A.M.; Hanson R.W.  
AN 1992:22306506 BIOTECHNO

L177 ANSWER 29 OF 75 BIOTECHNO COPYRIGHT 2000 Elsevier Science B.V.  
TI Analysis of **mutations** that uncouple **transport** from  
phosphorylation in enzyme II(Glc) of the Escherichia coli  
**phosphoenolpyruvate**-dependent **phosphotransferase** system  
SO Journal of Bacteriology, (1992), 174/9 (2843-2850)  
CODEN: JOBAAY ISSN: 0021-9193

AU Ruijter G.J.G.; Van Meurs G.; Verwey M.A.; Postma P.W.; Van Dam K.  
AN 1992:22184632 BIOTECHNO

L177 ANSWER 30 OF 75 BIOTECHNO COPYRIGHT 2000 Elsevier Science B.V.  
TI Factors affecting the manganese and iron activation of the  
**phosphoenolpyruvate** carboxykinase isozymes from rabbit  
SO Biochimica et Biophysica Acta - General Subjects, (1992),

1156/1 (85-91)  
CODEN: BBGSB3 ISSN: 0304-4165  
AU lambeth D.O.; Muhonen W.W.; Jacoby G.H.; Ray P.D.  
AN 1992:23004910 BIOTECHNO

L177 ANSWER 31 OF 75 BIOTECHNO COPYRIGHT 2000 Elsevier Science B.V.  
TI Insertion of the mannitol permease into the membrane of *Escherichia coli*:  
Possible involvement of an N-terminal amphiphilic sequence  
SO *Journal of Biological Chemistry*, (1991), 266/27 (17863-17871)  
CODEN: JBCHA3 ISSN: 0021-9258  
AU Yamada Y.; Chang Y.-Y.; Daniels G.A.; Wu L.-F.; Tomich J.M.; Yamada M.;  
Saier Jr. M.H.  
AN 1991:21332664 BIOTECHNO

L177 ANSWER 32 OF 75 BIOTECHNO COPYRIGHT 2000 Elsevier Science B.V.  
TI Secondary structure of the phosphocarrier protein III(Glc), a signal-  
transducing protein from *Escherichia coli*, determined by heteronuclear  
three-dimensional NMR spectroscopy  
SO *Proceedings of the National Academy of Sciences of the United States of*  
*America*, (1991), 88/8 (3479-3483)  
CODEN: PNASA6 ISSN: 0027-8424  
AU Pelton J.G.; Torchia D.A.; Meadow N.D.; Wong C.-Y.; Roseman S.  
AN 1991:22072878 BIOTECHNO

L177 ANSWER 33 OF 75 BIOTECHNO COPYRIGHT 2000 Elsevier Science B.V.  
TI The **glucose** permease of the **phosphotransferase** system  
of *Bacillus subtilis*: Evidence for II(Glc) and III(Glc) domains  
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1	L1	2792	carbon near2 (flux or flow)	USPAT	2000/06/21 09:22
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3	L3	100	(phosphoenol adj pyruvate or pep or phosphoenolpyruvate or phospho adj enol adj pyruvate) near4 (suppl\$4 or availab\$8)	USPAT	2000/06/21 09:41
4	L4	2	2 and 3	USPAT	2000/06/21 09:41

USPT

US-CL-CURRENT: 435/108, 435/200, 536/23.7, 536/24.1

US-PAT-NO: 5985617

DOCUMENT-IDENTIFIER: US 5985617 A

TITLE: Microorganisms and methods for overproduction of DAHP by cloned PPS gene

DATE-ISSUED: November 16, 1999

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Liao; James C.	Los Angeles	CA	90024	N/A

US-CL-CURRENT: 435/72, 435/108, 435/200, 536/23.7, 536/24.1

ABSTRACT:

Genetic elements comprising expression vectors and a gene coding for phosphoenol pyruvate synthase is utilized to enhance diversion of carbon resources into the common aromatic pathway and pathways branching therefrom. The overexpression of phosphoenol pyruvate synthase increases DAHP production to near theoretical yields.

29 Claims, 14 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 6

BSPR:

The overproduction of transketolase in tkt transformed cells has been found to provide an increased flow of carbon resources into the common aromatic pathway relative to carbon resource utilization in whole cells that do not harbor such genetic elements. However, the increased carbon flux may be further enhanced by additional manipulation of the host strain.

BSPR:

The present invention further provides a method for increasing carbon flow for the biosynthesis of DAHP in a host cell comprising the steps of transforming into the host cell recombinant DNA comprising a pps gene so that Pps is expressed at enhanced levels relative to wild type host cells, concentrating the transformed cells through centrifugation, resuspending the cells in a minimal, nutrient lean medium, fermenting the resuspended cells, and isolating DAHP from the medium.

BSPR:

The present invention further provides methods of increasing carbon flow into the common aromatic pathway of a host cell comprising the step of transforming the host cell with recombinant DNA comprising a pps gene so that Pps is expressed at appropriate point in the metabolic pathways at enhanced levels relative to wild type host cells.

DEPR:

The inventor have found that cell lines can be developed that increase the carbon flux into DAHP production and achieve near theoretical yields of DAHP by overexpressing phosphoenolpyruvate synthase (Pps) in the cell lines. Overexpression of Pps can increase the final concentration and yield of DAHP by as much as two-fold, to a near theoretical maximum as compared to wild type cell lines. The overexpression of Pps is achieved by transforming a cell line with recombinant DNA comprising a pps gene so that Pps is expressed at enhanced level relative to the wild type cell line and so that the yield of DAHP approaches its theoretical value.

DEPR:

Besides the use of the pps gene, the present invention also provides for transfer of genetic elements comprising the tkt gene, the gene coding for DAHP synthase (aroF in *E. coli*), the gene coding for 3-dehydroquinate synthase (aroB in *E. coli*), or other genes encoding enzymes that catalyze reactions in the common aromatic pathway. Such a cell transformation can be achieved by transferring one or more plasmids that contain genes that code for enzymes that increase the carbon flux for DAHP synthesis and for subsequent synthesis of

other desired cyclic, pre-aromatic, and aromatic metabolites. As a result of this transfer of genetic element(s), more carbon enters and moves through the common aromatic pathway relative to wild type host cells not containing the genetic elements of the present invention.

DEPR:

In one embodiment, the present invention comprises a method for increasing carbon flow into the common aromatic pathway of a host cell by increasing the production of DAHP through the overexpression of Pps at the appropriate point in the common aromatic pathway to provide additional PEP at the point where PEP condenses with E4P. Increasing carbon flow requires the step of transforming the host cell with recombinant DNA containing a pps genes so that Pps is overexpressed at enhanced levels relative to wild type host cells. DAHP is then produced by fermentation of the transformed cell in a nutrient medium which the DAHP can be extracted from the medium on a batch wise or continuous extraction procedure.

DEPR:

Another embodiment of the present invention is a method for enhancing a host cell's biosynthetic production of compounds derived from the common aromatic pathway. This method involves the step of increasing expression of Pps in the host cell relative to a wild type host cell. The step of increasing expression of Pps can include transferring into the host cell a vector carrying the pps gene. The overexpression of Pps results in forcing increased carbon flow into the biosynthesis of DAHP.

DEPR:

Besides being used in the biosynthesis of DAHP, PEP is used as a phosphate donor in the phosphotransferase system (PTS) which is responsible for glucose uptake. Additionally, PEP can be converted to pyruvate by pyruvate kinases and to oxaloacetate by phosphoenolpyruvate carboxylase. All such competing pathways limit the availability of PEP for the biosynthesis of DAHP and all metabolites derived from the common aromatic pathway or pathways branching therefrom.

DEPR:

A key component of the methods of the present invention directed at increased carbon flux commitment to DAHP and DAHP metabolites is the recycling of pyruvate to PEP. Pyruvate is available in host cells as an end product of glycolysis.

DEPR:

This example demonstrates that the *E. coli* AB2847 is unable to utilize DAHP, and accumulates DAHP in the medium if DAHP synthase is overexpressed. This strain was used as a host for detecting the flux committed to the aromatic pathways. Since Draths et al. (Draths, K. M., D. L. Pompliano, D. L. Conley, J. W. Frost, A. Berry, G. L. Disbrow, R. J. Staversky, and J. C. Lievense, "Biocatalytic synthesis of aromatics from D-glucose: The role of transketolase," *J. Am. Chem. Soc.*, 1992, 114, 3956-3962) have shown a possible limitation in the production of DAHP by E4P, pAT1 (containing both aroG.sup.fbr and tktA) was transformed into AB2847 to eliminate the limitation of E4P. To test whether PEP supply limits DAHP production, PEP synthase (Pps) was overexpressed in AB2847/pAT1 by transforming plasmid pPS341 into this strain. 20-70 copies of the pps gene were expressed in the host cells. As a control, pPS341 was substituted by pPS341X1, which encodes an inactive, but stable pps gene product. The use of the inactive Pps control allowed discrimination between the effect of Pps activity and that of protein overexpression. AB2847/pAT1/pUHE23-2 and AB2847/pAT1 were also used without any other plasmid as additional controls to identify the effect of the cloning vector, pUHE23-2, on DAHP production.

DEPR:

To determine whether the Pps effect requires overexpressed transketolase (Tkt) as well, plasmid pRW5, which contains only aroG.sup.fbr, was used in place of pAT1 in the above experiments. It was found that overproduction of Pps did not increase the DAHP production (FIG. 2A) without the elevated Tkt activity. Therefore, as limitation of small molecules in the biosynthesis of DAHP is concerned, the first limitation arises from the supply of E4P. This bottleneck

shifts to the supply of PEP when Tkt is overexpressed, which is believed to increase the supply of E4P.

DEPR:

Since PEP is also converted to OAA by Ppc, the deletion of this enzyme may increase the supply of PEP. Therefore, the ppc gene on the chromosome of AB2847 was inactivated to determine whether DAHP production could be increased without Pps overexpression. This was done by transducing AB2847 with a P1 lysate grown on JCL1242 ppc::Km. The resulting transductant, JCL1283 aroB ppc::Km was then transformed with pAT1 or pRW5 and tested for DAHP production in the re-suspension culture as described above. To avoid limitation of OAA in the ppc strain, the culture medium was supplemented with succinate, which was shown to have no effect on DAHP production (data not shown). Contrary to the expectation, ppc mutation did not increase the production of DAHP (FIG. 2B), suggesting that the metabolic flux from PEP to OAA was not significant under the experimental conditions tested here. In fact, the ppc mutation actually decreased the DAHP production for unknown reasons.

USPT

US-CL-CURRENT: 435/108, 435/200, 536/23.7, 536/24.1

US-PAT-NO: 5906925

DOCUMENT-IDENTIFIER: US 5906925 A

TITLE: Microorganisms and methods for overproduction of DAHP by cloned pps gene

DATE-ISSUED: May 25, 1999

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Liao, James C.	N/A	N/A	N/A	N/A
	College Station	TX	77843-312	

2

US-CL-CURRENT: 435/72, 435/108, 435/200, 536/23.7, 536/24.1

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DEPR:

Besides the use of the pps gene, the present invention also provides for transfer of genetic elements comprising the tkt gene, the gene coding for DAHP synthase (aroF in E. coli), the gene coding for 3-dehydroquinate synthase (aroB in E. coli), or other genes encoding enzymes that catalyze reactions in the common aromatic pathway. Such a cell transformation can be achieved by

transferring one or more plasmids that contain genes that code for enzymes that increase the carbon flux for DAHP synthesis and for subsequent synthesis of other desired cyclic, pre-aromatic, and aromatic metabolites. As a result of this transfer of genetic element(s), more carbon enters and moves through the common aromatic pathway relative to wild type host cells not containing the genetic elements of the present invention.

DEPR:

In one embodiment, the present invention comprises a method for increasing carbon flow into the common aromatic pathway of a host cell by increasing the production of DAHP through the overexpression of Pps at the appropriate point in the common aromatic pathway to provide additional PEP at the point where PEP condenses with E4P. Increasing carbon flow requires the step of transforming the host cell with recombinant DNA containing a pps gene so that Pps is overexpressed at enhanced levels relative to wild type host cells. DAHP is then produced by fermentation of the transformed cell in a nutrient medium from which the DAHP can be extracted from the medium on a batch wise or continuous extraction procedure.

DEPR:

Another embodiment of the present invention is a method for enhancing a host cell's biosynthetic production of compounds derived from the common aromatic pathway. This method involves the step of increasing expression of Pps in the host cell relative to a wild type host cell. The step of increasing expression of Pps can include transferring into the host cell a vector carrying the pps gene. The overexpression of Pps results in forcing increased carbon flow into the biosynthesis of DAHP.

DEPR:

Besides being used in the biosynthesis of DAHP, PEP is used as a phosphate donor in the phosphotransferase system (PTS) which is responsible for glucose uptake. Additionally, PEP can be converted to pyruvate by pyruvate kinases and to oxaloacetate by phosphoenolpyruvate carboxylase. All such competing pathways limit the availability of PEP for the biosynthesis of DAHP and all metabolites derived from the common aromatic pathway or pathways branching therefrom.

DEPR:

A key component of the methods of the present invention directed at increased carbon flux commitment to DAHP and DAHP metabolites is the recycling of pyruvate to PEP. Pyruvate is available in host cells as an end product of glycolysis.

DEPR:

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DEPR:

To determine whether the Pps effect requires overexpressed transketolase (Tkt) as well, plasmid PRW5, which contains only aroG.sup.fbr, was used in place of pAT1 in the above experiments. It was found that overproduction of Pps did not increase the DAHP production (FIG. 2A) without the elevated Tkt activity.

Therefore, as limitation of small molecules in the biosynthesis of DAHP is concerned, the first limitation arises from the supply of E4P. This bottleneck shifts to the supply of PEP when Tkt is overexpressed, which is believed to increase the supply of E4P.

DEPR:

Since PEP is also converted to OAA by Ppc, the deletion of this enzyme may increase the supply of PEP. Therefore, the ppc gene on the chromosome of AB2847 was inactivated to determine whether DAHP production could be increased without Pps overexpression. This was done by transducing AB2847 with a P1 lysate grown on JCL1242 ppc::Km. The resulting transductant, JCL1283 aroB ppc::Km was then transformed with pAT1 or pRW5 and tested for DAHP production in the re-suspension culture as described above. To avoid limitation of OAA in the ppc strain, the culture medium was supplemented with succinate, which was shown to have no effect on DAHP production (data not shown). Contrary to the expectation, ppc mutation did not increase the production of DAHP (FIG. 2B), suggesting that the metabolic flux from PEP to OAA was not significant under the experimental conditions tested here. In fact, the ppc mutation actually decreased the DAHP production for unknown reasons.

	L #	Hits	Search Text	DBs	Time Stamp
1	L1	2792	carbon near2 (flux or flow)	USPAT	2000/06/21 09:22
2	L2	133	1 near4 (modif\$8 or alter\$8 or increas\$8)	USPAT	2000/06/21 09:25
3	L3	100	(phosphoenol adj pyruvate or pep or phosphoenolpyruvate or phospho adj enol adj pyruvate) near4 (suppl\$4 or availab\$8)	USPAT	2000/06/21 09:41
4	L4	2	2 and 3	USPAT	2000/06/21 09:51
5	L5	2011	phosphotransferase\$1 or phospho adj transferase\$1	USPAT	2000/06/21 09:53
6	L6	6	(2 or 3) and 5	USPAT	2000/06/21 09:58
7	L7	16	(2 or 3) same (aromatic or shikimate)	USPAT	2000/06/21 09:59

USPT

US-CL-CURRENT: 435/108, 435/200, 536/23.7, 536/24.1

US-PAT-NO: 5985617

DOCUMENT-IDENTIFIER: US 5985617 A

TITLE: Microorganisms and methods for overproduction of DAHP by cloned PPS gene

DATE-ISSUED: November 16, 1999

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Liao; James C.	Los Angeles	CA	90024	N/A

US-CL-CURRENT: 435/72, 435/108, 435/200, 536/23:7, 536/24.1

ABSTRACT:

Genetic elements comprising expression vectors and a gene coding for phosphoenol pyruvate synthase is utilized to enhance diversion of carbon resources into the common aromatic pathway and pathways branching therefrom. The overexpression of phosphoenol pyruvate synthase increases DAHP production to near theoretical yields.

29 Claims, 14 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 6

BSPR:

The overproduction of transketolase in tkt transformed cells has been found to provide an increased flow of carbon resources into the common aromatic pathway relative to carbon resource utilization in whole cells that do not harbor such genetic elements. However, the increased carbon flux may be further enhanced by additional manipulation of the host strain.

BSPR:

The present invention further provides a method for increasing carbon flow for the biosynthesis of DAHP in a host cell comprising the steps of transforming into the host cell recombinant DNA comprising a pps gene so that Pps is expressed at enhanced levels relative to wild type host cells, concentrating the transformed cells through centrifugation, resuspending the cells in a minimal, nutrient lean medium, fermenting the resuspended cells, and isolating DAHP from the medium.

BSPR:

The present invention further provides methods of increasing carbon flow into the common aromatic pathway of a host cell comprising the step of transforming the host cell with recombinant DNA comprising a pps gene so that Pps is expressed at appropriate point in the metabolic pathways at enhanced levels relative to wild type host cells.

DEPR:

The inventor have found that cell lines can be developed that increase the carbon flux into DAHP production and achieve near theoretical yields of DAHP by overexpressing phosphoenolpyruvate synthase (Pps) in the cell lines. Overexpression of Pps can increase the final concentration and yield of DAHP by as much as two-fold, to a near theoretical maximum as compared to wild type cell lines. The overexpression of Pps is achieved by transforming a cell line with recombinant DNA comprising a pps gene so that Pps is expressed at enhanced level relative to the wild type cell line and so that the yield of DAHP approaches its theoretical value.

DEPR:

Besides the use of the pps gene, the present invention also provides for transfer of genetic elements comprising the tkt gene, the gene coding for DAHP synthase (aroF in *E. coli*), the gene coding for 3-dehydroquinate synthase (aroB in *E. coli*), or other genes encoding enzymes that catalyze reactions in the common aromatic pathway. Such a cell transformation can be achieved by transferring one or more plasmids that contain genes that code for enzymes that increase the carbon flux for DAHP synthesis and for subsequent synthesis of

other desired cyclic, pre-aromatic, and aromatic metabolites. As a result of this transfer of genetic element(s), more carbon enters and moves through the common aromatic pathway relative to wild type host cells not containing the genetic elements of the present invention.

DEPR:

In one embodiment, the present invention comprises a method for increasing carbon flow into the common aromatic pathway of a host cell by increasing the production of DAHP through the overexpression of Pps at the appropriate point in the common aromatic pathway to provide additional PEP at the point where PEP condenses with E4P. Increasing carbon flow requires the step of transforming the host cell with recombinant DNA containing a pps genes so that Pps is overexpressed at enhanced levels relative to wild type host cells. DAHP is then produced by fermentation of the transformed cell in a nutrient medium which the DAHP can be extracted from the medium on a batch wise or continuous extraction procedure.

DEPR:

Another embodiment of the present invention is a method for enhancing a host cell's biosynthetic production of compounds derived from the common aromatic pathway. This method involves the step of increasing expression of Pps in the host cell relative to a wild type host cell. The step of increasing expression of Pps can include transferring into the host cell a vector carrying the pps gene. The overexpression of Pps results in forcing increased carbon flow into the biosynthesis of DAHP.

DEPR:

Besides being used in the biosynthesis of DAHP, PEP is used as a phosphate donor in the phosphotransferase system (PTS) which is responsible for glucose uptake. Additionally, PEP can be converted to pyruvate by pyruvate kinases and to oxaloacetate by phosphoenolpyruvate carboxylase. All such competing pathways limit the availability of PEP for the biosynthesis of DAHP and all metabolites derived from the common aromatic pathway or pathways branching therefrom.

DEPR:

A key component of the methods of the present invention directed at increased carbon flux commitment to DAHP and DAHP metabolites is the recycling of pyruvate to PEP. Pyruvate is available in host cells as an end product of glycolysis.

DEPR:

As shown in FIG. 3A, for maximum yield of DAHP production by strains without Pps overproduction, 7 moles of glucose are needed to produce 3 moles of DAHP (43% molar yield) and 7 moles of pyruvate which is further metabolized. The relative flux through each intermediate step is also shown in FIG. 3A. The formation of pyruvate is necessary because of the stoichiometry of the phosphotransferase system for glucose uptake.

DEPR:

The stimulation of glucose consumption in the previous work was attributed to the altered PEP/pyruvate ratio. It was hypothesized that increased PEP/pyruvate ratio stimulates the phosphotransferase system for increased glucose consumption, which in turn results in the excretion of pyruvate.

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USPT

US-CL-CURRENT: 435/108, 435/200, 536/23.7, 536/24.1

US-PAT-NO: 5906925

DOCUMENT-IDENTIFIER: US 5906925 A

TITLE: Microorganisms and methods for overproduction of DAHP by cloned pps gene

DATE-ISSUED: May 25, 1999

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Liao; James C.	N/A	N/A	N/A	N/A
	College Station	TX	77843-312	
			2	

US-CL-CURRENT: 435/72, 435/108, 435/200, 536/23.7, 536/24.1

ABSTRACT:

Genetic elements comprising expression vectors and a gene coding for phosphoenol pyruvate synthase is utilized to enhance diversion of carbon resources into the common aromatic pathway and pathways branching therefrom. The overexpression of phosphoenol pyruvate synthase increases DAHP production to near theoretical yields.

28 Claims, 14 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 6

BSPR:

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BSPR:

The present invention further provides a method for increasing carbon flow for the biosynthesis of DAHP in a host cell comprising the steps of transforming into the host cell recombinant DNA comprising a pps gene so that Pps is expressed at enhanced levels relative to wild type host cells, concentrating the transformed cells through centrifugation, resuspending the cells in a minimal, nutrient lean medium, fermenting the resuspended cells, and isolating DAHP from the medium.

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Another embodiment of the present invention is a method for enhancing a host cell's biosynthetic production of compounds derived from the common aromatic pathway. This method involves the step of increasing expression of Pps in the host cell relative to a wild type host cell. The step of increasing expression of Pps can include transferring into the host cell a vector carrying the pps gene. The overexpression of Pps results in forcing increased carbon flow into the biosynthesis of DAHP.

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overexpressed in AB2847/pAT1 by transforming plasmid pPS341 into this strain. 20-70 copies of the pps gene were expressed in the host cells. As a control, pPS341 was substituted by pPS341X1, which encodes an inactive, but stable pps gene product. The use of the inactive Pps control allowed discrimination between the effect of Pps activity and that of protein overexpression. AB2847/pAT1/pUHE23-2 and AB2847/pAT1 were also used without any other plasmid as additional controls to identify the effect of the cloning vector, pUHE23-2, on DAHP production.

DEPR:

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USPT

US-CL-CURRENT: 530/370,536/23.6 ,800/278 ,800/290 ,800/298

US-PAT-NO: 5891726

DOCUMENT-IDENTIFIER: US 5891726 A

TITLE: Procedure to increase the seed productivity of plants and to accelerate the growth of plants by means of an additional plastidic pyruvate, phosphate dikinase

DATE-ISSUED: April 6, 1999

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Sheriff; Ahmed	D-12305 Berlin	N/A	N/A	DEX

US-CL-CURRENT: 435/419,530/370 ,536/23.6 ,800/278 ,800/290 ,800/298

ABSTRACT:

The present invention includes novel methods for increasing the seed productivity or accelerating the growth rate of a plant and plants produced by such methods. Such plants have at least one cell transformed with an expression complex comprising a promoter operably linked to a gene encoding a pyruvate phosphate dikinase which is capable of converting pyruvate into phosphoenolpyruvate. The plants are made by transforming at least one plant cell with an appropriate expression construct, regenerating plants from one or more transformed plant cells and selecting at least one plant having the desired phenotype.

7 Claims, 16 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 8

BSPR:

Latzko and Kelly (1983) suggested another ten biochemical reason for the occurrence of PEPCase. But, these other purposes do not bring about immediate energetical advantages. Phosphoenolpyruvate is a substrate for PEPCase. It can, for example, be generated from pyruvate by PPDK and, maybe PEPCase is limited by the supply of phosphoenolpyruvate. The enzymatic characteristics and metabolic functions of PPDK from non-photosynthetically active tissues are only poorly understood (Fi.beta.lthaler et al. 1995; Rosche et al. 1994).

DRPR:

FIG. 3: Schematic drawing of the binary vectors with the *M. crystallinum* PPDK-insertion. .DELTA. represents a deletion of 183 bp at the 5'-end. The PPDK cDNA-sequence from *M. crystallinum* is 3173 bp long (Fi.beta.lthaler et al. 1995). The transnational start-codon is at position 63. The termination codon is at position 1920. The protein deduced from the cDNA sequence contains 949 amino acids (aa), which corresponds to a relative molecular mass (M.sub.r) of 103244 daltons. The presequence has a length of 74 aa. The mature plastidic enzyme has a M.sub.r of 94 kDa. 5'- and 3'-untranslated parts of the cDNA are indicated as terminal hatched boxes (left 5', right 3'-untranslated region; the dotted box represents the plastid presequence with three ATGs in the open reading frame). The T-DNA contained a neomycin phosphotransferase (nptII, kanamycin resistance) with plant regulatory elements. 35S CaMV: promoter of the cauliflower mosaic virus; ocs polyA: polyadenylation signal of the octopin synthase gene from *A. tumefaciens*; BR, BL: right, left borders of the T-DNA of *Agrobacterium tumefaciens*; Km: kanamycin resistance with prokaryotic regulational elements (Beven 1984). Transformation of the tobacco plants by *A. tumefaciens* was performed according to Horsch et al. (1985).

USPT

US-CL-CURRENT: 435/419, 435/468, 435/469, 435/69.1, 536/23.2, 536/23.6  
, 536/24.1

US-PAT-NO: 5856177

DOCUMENT-IDENTIFIER: US 5856177 A

TITLE: Promoters derived from the maize phosphoenolpyruvate carboxylase gene involved in C.sub.4 photosynthesis

DATE-ISSUED: January 5, 1999

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Grula; John W.	Pasadena	CA	N/A	N/A
Hudspeth; Richard L.	Altadena	CA	N/A	N/A

US-CL-CURRENT: 435/320.1, 435/419, 435/468, 435/469, 435/69.1, 536/23.2  
, 536/23.6, 536/24.1

ABSTRACT:

A plasmid comprising a phosphoenolpyruvate carboxylase gene and promoter isolated from maize. The phosphoenolpyruvate carboxylase gene encodes a phosphoenolpyruvate carboxylase isozyme involved in C.sub.4 photosynthesis and which is not expressed in seeds.

6 Claims, 36 Drawing figures

Exemplary Claim Number: 2

Number of Drawing Sheets: 30

DEPR:

Alternatively, the suspension may be resuspended in fresh medium containing cefotaxime and allowed to grow an additional 4 to 28 days prior plating on solidified medium in Petri dishes. Cell concentration is 1 vol. of suspension cells plus 3 vol. of medium with cefotaxime. Kanamycin at 10 to 300 mg/l preferably about 20 to 200 mg/l more preferably about 40 to 80 mg/l is included in the medium for selection of transformed cells expressing the neomycin phosphotransferase (NPT) gene. Cells and embryos proliferating in the selective concentration of kanamycin are further grown as set forth above to mature somatic embryos capable of germinating and regenerating into whole plants according to the procedures described herein.

DEPR:

Immunoprecipitation of in vitro translation products with *Staphylococcus aureus* Cowan 1 strain cells (IgGsorb supplied by The Enzyme Center, Boston, Mass.) was performed as described by Cullen et al. (1976) J. Immunol. 117 136-142, which is incorporated herein by reference. Antibodies against maize PEP carboxylase (supplied by Sigma Chemical Corp. St Louis, Mo.) were prepared by Antibodies Inc. (Davis, Calif.). Proteins were analyzed by SDS polyacrylamide gel electrophoresis in 5-15% gradient slab gels run at 3 V/cm for 16 hr. The gels were treated with EN.sup.3 HANCE (supplied by New England Nuclear), dried and exposed for 16-72 hr to X-ray film at -70.degree. C. with an intensifying screen.

DEPR:

Two T-DNA PstI cleaved right border sequences from *A. tumefaciens* (strain C-58) were further subdivided with BamHI for integration in the plant genome, a passenger maize phosphoenolpyruvate carboxylase gene described above as the insert of H1.lambd.a.14, and a chimeric gene (NOS/NPT/TK) capable of expression in plants and conferring resistance to the antibiotics kanamycin and G418 were ligated into pRK290 which contains a wide host range replicon required for replication in *A. tumefaciens*. This chimeric gene utilizes a nopaline synthetase promoter, the neomycin phosphotransferase II coding region from Tn5, and the terminator from the herpes simplex virus thymidine kinase gene. The resultant plasmid, designated DEI PEP 10, is shown in FIG. 33. The complete DEI PEP 10 is given in Hudspeth (1988, Ph.D. Thesis) and incorporated herein by reference.

DEPR:

The suspension culture as obtained in Example 12 was transformed using an Agrobacteria which contained the T-DNA containing binary vector pCIB10

[Rothstein et al., Gene 53 153-161 (1987), incorporated herein by reference] as well as the pAL4404 vir-plasmid. The T-DNA of pCIB10 contains a chimeric gene composed of the promoter from nopaline synthase, the coding region from Tn5 encoding the enzyme neomycin phosphotransferase, and the terminator from nopaline synthase. The Agrobacteria containing pCIB10 were grown on YEB medium containing kanamycin (50 .mu.g/ml). Transformation was accomplished in the same manner as in Example 13 except that the 1 ml aliquots resulting in cells and Agrobacteria were immediately plated on selective media containing either kanamycin (50 .mu.g/ml) or G418 (25 .mu.g/ml). Expression of the nos/neo/nos chimeric gene in transformed plant tissue allows the selection of this tissue in the presence of both antibiotics. The existence in two to four weeks of transformed tissue became apparent on the selection plates. Uninfected tissue as well as added control tissue showed no signs of growth, turned brown and died. Transformed tissue grew very well in the presence of both kanamycin and G418.

DEPR:

The procedure of Example 13 was followed, except that the transforming Agrobacteria used contained the T-DNA vector DEI PEP10 as well as the pAL4404 vir plasmid. DEI PEP10, shown in FIG. 33, utilizes two T-DNA PstI cleaved right border sequences from *A. tumefaciens* (strain C-58) which had been further subdivided with BamHI for integration in the plant genome, a passenger maize phosphoenolpyruvate carboxylase gene (Pepcase gene), and a chimeric gene (NOS/NPT/TK) capable of expression in plants and conferring resistance to the antibiotics kanamycin and G418. This chimeric gene utilizes a nopaline synthetase promoter, the neomycin phosphotransferase II coding region from Tn5, and the terminator from the herpes simplex virus thymidine kinase gene. Following transformation, embryogenic callus and embryos were obtained by selection on kanamycin (50 mg/l). No resistant callus was obtained from the control (non-transformed callus) plated on kanamycin at this level (50 mg/l).

DEPR:

The procedure of Example 13 was followed, except that the transforming Agrobacteria used contained the T-DNA vector pPMG85/587 [Fillatti et al., Mol. Genet. 206 192-199 (1987) incorporated herein by reference] as well as the pAL4404 vir plasmid. The plasmid pPMG85/587 carries three chimeric genes capable of expression in plants. Two genes code for neomycin phosphotransferase (NPT) which confers resistance to the antibiotics kanamycin and G418. The third chimeric gene, containing the coding sequence from a mutant aroA gene of *S. typhimurium*, confers tolerance to the herbicide glyphosate [Comai et al., Science 221 370-371 (1983), incorporated herein by reference]. The Agrobacteria containing pPMG85/587 were grown on medium containing kanamycin (100 .mu.g/ml). Transformation is accomplished as detailed in Example 13 except that the suspension is allowed to grow for 28 days at which time 1 ml aliquots were plated on medium containing selective antibiotics. Expression of the NPT chimeric gene in transformed plant tissue allowed selection of this tissue on both antibiotics. In this instance the selective antibiotic was kanamycin (50 .mu.g/ml).

DEPR:

The transformation procedure of Example 13 was followed except there was used as the transforming Agrobacteria one containing the T-DNA binary vector pCIB715 [Rothstein et al. Gene 53 153-161 (1987)] as well as the vir plasmid. The T-DNA of pCIB715 contains a chimeric gene composed of the promoter and terminator from the cauliflower mosaic virus (CaMV) 35S transcript [Odell et al., Nature 313 810-812 (1985), incorporated herein by reference] and the coding sequence for hygromycin B phosphotransferase [Gritz et al., Gene 25 179-188 (1983) incorporated herein by reference]. Agrobacteria containing pCIB715 was grown on YEB containing kanamycin (50 .mu.g/ml).

DEPR:

A plasmid containing the gene for expression of kanamycin resistance in plants was constructed (see FIGS. 22 and 23). Plasmid Bin6 obtained from Dr. M. Bevan, Plant Breeding Institute, Cambridge, UK. This plasmid is described in the reference by Bevan [Nucl. Acids Res. 12 8711-8721 (1984) incorporate herein by reference]. Plasmid Bin6 DNA was digested with EcoRI and HindIII and the fragment approximately 1.5 kb in size containing the chimeric neomycin phosphotransferase (NPT) gene is isolated and purified following agarose gel electrophoresis. This fragment was then mixed with plasmid pUC18 DNA which had

been cleaved with endonucleases EcoRI and HindIII. Following incubation with T4 DNA ligase, the resulting DNA was transformed into *E. coli* strain HB101. The resulting plasmid is called pUC18/neo. This plasmid DNA containing an unwanted BamHI recognition sequence between the neomycin phosphotransferase gene and the terminator sequence for nopaline synthase [see Bevan Nucl. Acids Res. 12 8711-8721 (1984) incorporated herein by reference]. To remove this recognition sequence, plasmid pUC18/neo was digested with endoruclease BamHI, followed by treatment with the large fragment of DNA polymerase to create flush ends. The fragment was then incubated with T4 DNA ligase to recircularize the fragment, and transformed into *E. coli* strain HB101. The resulting plasmid, pUC18/neo(Bam) has lost the BamHI recognition sequence.

	L #	Hits	Search Text	DBs	Time Stamp
1	L1	2792	carbon near2 (flux or flow)	USPAT	2000/06/21 09:22
2	L2	133	1 near4 (modif\$8 or alter\$8 or increas\$8)	USPAT	2000/06/21 09:25
3	L3	100	(phosphoenol adj pyruvate or pep or phosphoenolpyruvate or phospho adj enol adj pyruvate) near4 (suppl\$4 or availab\$8)	USPAT	2000/06/21 09:41
4	L4	2	2 and 3	USPAT	2000/06/21 09:51
5	L5	2011	phosphotransferase\$1 or phospho adj transferase\$1	USPAT	2000/06/21 09:53
6	L6	6	(2 or 3) and 5	USPAT	2000/06/21 09:58
7	L7	16	(2 or 3) same (aromatic or shikimate)	USPAT	2000/06/21 09:59

USPT

US-CL-CURRENT: 435/136, 435/146, 435/155, 435/156, 435/252.8, 435/317.1  
, 435/320.1, 435/849

US-PAT-NO: 6030819

DOCUMENT-IDENTIFIER: US 6030819 A

TITLE: Genetically engineered microorganisms and method for producing  
4-hydroxybenzoic acid

DATE-ISSUED: February 29, 2000

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Amaratunga; Mohan	Clifton Park	NY	N/A	N/A
Lobos; John Henry	Ballston Spa	NY	N/A	N/A
Johnson; Bruce Fletcher	Scotia	NY	N/A	N/A
Williams; Eric Douglas	Schenectady	NY	N/A	N/A

US-CL-CURRENT: 435/132, 435/136, 435/146, 435/155, 435/156, 435/252.8, 435/317.1  
, 435/320.1, 435/849

ABSTRACT:

The present invention pertains to a method for economical biofermentative production of 4-hydroxybenzoic acid (PHB) using genetically engineered *E. coli*. According to the invention, a plasmid is provided which controls the overexpression of chorismate pyruvate lyase, the bacterial enzyme which catalyzes the production of PHB from chorismate. Mutant *E. coli* selected with a unique two-step screening assay to overproduce chorismate have been transformed with this plasmid, providing a biocatalyst that efficiently converts glucose to PHB.

17 Claims, 3 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 3

DEPR:

In *E. coli*, transformation of glucose to PHB involves approximately fifteen different enzymatic steps. FIG. 1 provides a summary of the important intermediates in the pathway. The *ubiC* gene product, CPL, is a likely candidate for amplification because of the low product turnover of CPL, and because it exists at a major branch in the metabolic pathway. At this point in the biosynthetic pathway, CPL's substrate, chorismate, may be converted to PHB, to prephenic acid (PPA) and the aromatic amino acids, or to a variety of other products. Therefore, increasing the carbon flow of metabolism toward chorismate increases the substrate available for conversion into PHB, and also increases the substrate available to the aromatic amino acid pathway through PPA, and to other products. Thus, cells which produce more chorismate and thus more PHB also produce more aromatic amino acids.

USPT

US-CL-CURRENT: 435/108, 435/200, 536/23.7, 536/24.1

US-PAT-NO: 5985617

DOCUMENT-IDENTIFIER: US 5985617 A

TITLE: Microorganisms and methods for overproduction of DAHP by cloned PPS gene

DATE-ISSUED: November 16, 1999

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Liao, James C.	Los Angeles	CA	90024	N/A

US-CL-CURRENT: 435/72, 435/108, 435/200, 536/23.7, 536/24.1

ABSTRACT:

Genetic elements comprising expression vectors and a gene coding for phosphoenol pyruvate synthase is utilized to enhance diversion of carbon resources into the common aromatic pathway and pathways branching therefrom. The overexpression of phosphoenol pyruvate synthase increases DAHP production to near theoretical yields.

29 Claims, 14 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 6

BSPR:

The overproduction of transketolase in tkt transformed cells has been found to provide an increased flow of carbon resources into the common aromatic pathway relative to carbon resource utilization in whole cells that do not harbor such genetic elements. However, the increased carbon flux may be further enhanced by additional manipulation of the host strain.

BSPR:

The present invention further provides methods of increasing carbon flow into the common aromatic pathway of a host cell comprising the step of transforming the host cell with recombinant DNA comprising a pps gene so that Pps is expressed at appropriate point in the metabolic pathways at enhanced levels relative to wild type host cells.

DEPR:

Besides the use of the pps gene, the present invention also provides for transfer of genetic elements comprising the tkt gene, the gene coding for DAHP synthase (aroF in *E. coli*), the gene coding for 3-dehydroquinate synthase (aroB in *E. coli*), or other genes encoding enzymes that catalyze reactions in the common aromatic pathway. Such a cell transformation can be achieved by transferring one or more plasmids that contain genes that code for enzymes that increase the carbon flux for DAHP synthesis and for subsequent synthesis of other desired cyclic, pre-aromatic, and aromatic metabolites. As a result of this transfer of genetic element(s), more carbon enters and moves through the common aromatic pathway relative to wild type host cells not containing the genetic elements of the present invention.

DEPR:

In one embodiment, the present invention comprises a method for increasing carbon flow into the common aromatic pathway of a host cell by increasing the production of DAHP through the overexpression of Pps at the appropriate point in the common aromatic pathway to provide additional PEP at the point where PEP condenses with E4P. Increasing carbon flow requires the step of transforming the host cell with recombinant DNA containing a pps genes so that Pps is overexpressed at enhanced levels relative to wild type host cells. DAHP is then produced by fermentation of the transformed cell in a nutrient medium which the DAHP can be extracted from the medium on a batch wise or continuous extraction procedure.

DEPR:

Another embodiment of the present invention is a method for enhancing a host cell's biosynthetic production of compounds derived from the common aromatic

pathway. This method involves the step of increasing expression of Pps in the host cell relative to a wild type host cell. The step of increasing expression of Pps can include transferring into the host cell a vector carrying the pps gene. The overexpression of Pps results in forcing increased carbon flow into the biosynthesis of DAHP.

DEPR:

Besides being used in the biosynthesis of DAHP, PEP is used as a phosphate donor in the phosphotransferase system (PTS) which is responsible for glucose uptake. Additionally, PEP can be converted to pyruvate by pyruvate kinases and to oxaloacetate by phosphoenolpyruvate carboxylase. All such competing pathways limit the availability of PEP for the biosynthesis of DAHP and all metabolites derived from the common aromatic pathway or pathways branching therefrom.

DEPR:

This example demonstrates that the *E. coli* AB2847 is unable to utilize DAHP, and accumulates DAHP in the medium if DAHP synthase is overexpressed. This strain was used as a host for detecting the flux committed to the aromatic pathways. Since Draths et al. (Draths, K. M., D. L. Pompliano, D. L. Conley, J. W. Frost, A. Berry, G. L. Disbrow, R. J. Staversky, and J. C. Lievense, "Biocatalytic synthesis of aromatics from D-glucose: The role of transketolase," *J. Am. Chem. Soc.*, 1992, 114, 3956-3962) have shown a possible limitation in the production of DAHP by E4P, pAT1 (containing both aroG.sup.fbr and tktA) was transformed into AB2847 to eliminate the limitation of E4P. To test whether PEP supply limits DAHP production, PEP synthase (Pps) was overexpressed in AB2847/pAT1 by transforming plasmid pPS341 into this strain. 20-70 copies of the pps gene were expressed in the host cells. As a control, pPS341 was substituted by pPS341X1, which encodes an inactive, but stable pps gene product. The use of the inactive Pps control allowed discrimination between the effect of Pps activity and that of protein overexpression. AB2847/pAT1/pUHE23-2 and AB2847/pAT1 were also used without any other plasmid as additional controls to identify the effect of the cloning vector, pUHE23-2, on DAHP production.

USPT

US-CL-CURRENT: 435/108, 435/200, 536/23.7, 536/24.1

US-PAT-NO: 5906925

DOCUMENT-IDENTIFIER: US 5906925 A

TITLE: Microorganisms and methods for overproduction of DAHP by cloned pps gene

DATE-ISSUED: May 25, 1999

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Liao, James C.	N/A	N/A	N/A	N/A
	College Station	TX	77843-312	
			2	

US-CL-CURRENT: 435/72, 435/108, 435/200, 536/23.7, 536/24.1

ABSTRACT:

Genetic elements comprising expression vectors and a gene coding for phosphoenol pyruvate synthase is utilized to enhance diversion of carbon resources into the common aromatic pathway and pathways branching therefrom. The overexpression of phosphoenol pyruvate synthase increases DAHP production to near theoretical yields.

28 Claims, 14 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 6

BSPR:

The overproduction of transketolase in tkt transformed cells has been found to provide an increased flow of carbon resources into the common aromatic pathway relative to carbon resource utilization in whole cells that do not harbor such genetic elements. However, the increased carbon flux may be further enhanced by additional manipulation of the host strain.

BSPR:

The present invention further provides methods of increasing carbon flow into the common aromatic pathway of a host cell comprising the step of transforming the host cell with recombinant DNA comprising a pps gene so that Pps is expressed at appropriate point in the metabolic pathways at enhanced levels relative to wild type host cells.

DEPR:

Besides the use of the pps gene, the present invention also provides for transfer of genetic elements comprising the tkt gene, the gene coding for DAHP synthase (aroF in *E. coli*), the gene coding for 3-dehydroquinate synthase (aroB in *E. coli*), or other genes encoding enzymes that catalyze reactions in the common aromatic pathway. Such a cell transformation can be achieved by transferring one or more plasmids that contain genes that code for enzymes that increase the carbon flux for DAHP synthesis and for subsequent synthesis of other desired cyclic, pre-aromatic, and aromatic metabolites. As a result of this transfer of genetic element(s), more carbon enters and moves through the common aromatic pathway relative to wild type host cells not containing the genetic elements of the present invention.

DEPR:

In one embodiment, the present invention comprises a method for increasing carbon flow into the common aromatic pathway of a host cell by increasing the production of DAHP through the overexpression of Pps at the appropriate point in the common aromatic pathway to provide additional PEP at the point where PEP condenses with E4P. Increasing carbon flow requires the step of transforming the host cell with recombinant DNA containing a pps gene so that Pps is overexpressed at enhanced levels relative to wild type host cells. DAHP is then produced by fermentation of the transformed cell in a nutrient medium from which the DAHP can be extracted from the medium on a batch wise or continuous extraction procedure.

DEPR:

Another embodiment of the present invention is a method for enhancing a host cell's biosynthetic production of compounds derived from the common aromatic pathway. This method involves the step of increasing expression of Pps in the host cell relative to a wild type host cell. The step of increasing expression of Pps can include transferring into the host cell a vector carrying the pps gene. The overexpression of Pps results in forcing increased carbon flow into the biosynthesis of DAHP.

DEPR:

Besides being used in the biosynthesis of DAHP, PEP is used as a phosphate donor in the phosphotransferase system (PTS) which is responsible for glucose uptake. Additionally, PEP can be converted to pyruvate by pyruvate kinases and to oxaloacetate by phosphoenolpyruvate carboxylase. All such competing pathways limit the availability of PEP for the biosynthesis of DAHP and all metabolites derived from the common aromatic pathway or pathways branching therefrom.

DEPR:

This example demonstrates that the *E. coli* AB2847 is unable to utilize DAHP, and accumulates DAHP in the medium if DAHP synthase is overexpressed. This strain was used as a host for detecting the flux committed to the aromatic pathways. Since Draths et al. (Draths, K. M., D. L. Pompliano, D. L. Conley, J. W. Frost, A. Berry, G. L. Disbrow, R. J. Staversky, and J. C. Lievense, "Biocatalytic synthesis of aromatics from D-glucose: The role of transketolase," *J. Am. Chem. Soc.*, 1992, 114, 3956-3962) have shown a possible limitation in the production of DAHP by E4P, pAT1 (containing both *aroG.sup.fbr* and *tktA*) was transformed into AB2847 to eliminate the limitation of E4P. To test whether PEP supply limits DAHP production, PEP synthase (Pps) was overexpressed in AB2847/pAT1 by transforming plasmid pPS341 into this strain. 20-70 copies of the pps gene were expressed in the host cells. As a control, pPS341 was substituted by pPS341X1, which encodes an inactive, but stable pps gene product. The use of the inactive Pps control allowed discrimination between the effect of Pps activity and that of protein overexpression. AB2847/pAT1/pUHE23-2 and AB2847/pAT1 were also used without any other plasmid as additional controls to identify the effect of the cloning vector, pUHE23-2, on DAHP production.

USPT

US-CL-CURRENT: 536/23.2

US-PAT-NO: 5866396

DOCUMENT-IDENTIFIER: US 5866396 A

TITLE: Microbial production of indigo

DATE-ISSUED: February 2, 1999

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Weyler; Walter	San Francisco	CA	94131	N/A
Dodge; Timothy C.	Rochester	NY	14617	N/A
Lauff; John J.	Rochester	NY	14612	N/A
Wendt; Dan J.	San Mateo	CA	94401	N/A

US-CL-CURRENT: 435/195, 536/23.2

ABSTRACT:

There is provided an improved process for the biosynthetic production of indigo, the improvement comprising removing unwanted by-products such as isatin or indirubin from the broth in which such indigo is produced. Isatin can be removed by enzymatic activity using an isatin-removing enzyme such as an isatin hydrolase, or by other techniques such as process parameters (elevated temperature, pH), or by contacting the broth containing the isatin with appropriate adsorption compounds/compositions such as carbon or appropriate resins. Since isatin is the precursor of indirubin, the indirubin levels are decreased as a result of isatin removal.

3 Claims, 16 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 13

BSPR:

Tryptophan pathway genes useful in securing biosynthetic indole accumulation include a trp operon, isolated from a microorganism as a purified DNA molecule that encodes an enzymatic pathway capable of directing the biosynthesis of L-tryptophan from chorismic acid. (A. J. Pittard (1987) Biosynthesis of Aromatic Amino Acids in *Escherichia coli* and *Salmonella typhimurium*, F. C. Neidhardt, ed., American Society for Microbiology, publisher, pp. 368-394.) Indole accumulation is enabled by modification of one or more of the pathway's structural elements and/or regulatory regions. This modified trp operon may then be introduced into a suitable host such as a microorganism, plant tissue culture system or other suitable expression system. It should be noted that the term "indole accumulation" does not necessarily indicate that indole actually accumulates intracellularly. Instead, this term can indicate that there is an increased flux of carbon to indole and indole is made available as a substrate for intracellular catalytic reactions such as indoxyl formation and other than the formation of L-tryptophan. In the context of this invention, the "accumulated" indole may be consumed in the conversion of indole to indoxyl by an oxygenase such as the aromatic dioxygenase NDO, or an aromatic monooxygenase such as TMO, or it may actually build up intracellularly and extracellularly, as would be the case when the desired end product is indole or one of its derivatives.